

# SEQUENCE LISTING

<110> Schneider, Michael  
Oh, Hidemasa

<120> Modulators of Telomere Stability

<130> HO-P02673US1

<140> Not Assigned

<141> 2004-04-08

<150> US 60/461,095

<151> 2003-04-08

<160> 24

<170> PatentIn version 3.1

<210> 1

<211> 500

<212> PRT

<213> Human

<400> 1

Met Ala Gly Gly Gly Gly Ser Ser Asp Gly Ser Gly Arg Ala Ala Gly  
1 5 10 15

Arg Arg Ala Ser Arg Ser Ser Gly Arg Ala Arg Arg Gly Arg His Glu  
20 25 30

Pro Gly Leu Gly Gly Pro Ala Glu Arg Gly Ala Gly Glu Ala Arg Leu  
35 40 45

Glu Glu Ala Val Asn Arg Trp Val Leu Lys Phe Tyr Phe His Glu Ala  
50 55 60

Leu Arg Ala Phe Arg Gly Ser Arg Tyr Gly Asp Phe Arg Gln Ile Arg  
65 70 75 80

Asp Ile Met Gln Ala Leu Leu Val Arg Pro Leu Gly Lys Glu His Thr  
85 90 95

Val Ser Arg Leu Leu Arg Val Met Gln Cys Leu Ser Arg Ile Glu Glu  
100 105 110

Gly Glu Asn Leu Asp Cys Ser Phe Asp Met Glu Ala Glu Leu Thr Pro  
115 120 125

Leu Glu Ser Ala Ile Asn Val Leu Glu Met Ile Lys Thr Glu Phe Thr  
130 135 140

Leu Thr Glu Ala Val Val Glu Ser Ser Arg Lys Leu Val Lys Glu Ala  
 145 150 155 160

Ala Val Ile Ile Cys Ile Lys Asn Lys Glu Phe Glu Lys Ala Ser Lys  
 165 170 175

Ile Leu Lys Lys His Met Ser Lys Asp Pro Thr Thr Gln Lys Leu Arg  
 180 185 190

Asn Asp Leu Leu Asn Ile Ile Arg Glu Lys Asn Leu Ala His Pro Val  
 195 200 205

Ile Gln Asn Phe Ser Tyr Glu Thr Phe Gln Gln Lys Met Leu Arg Phe  
 210 215 220

Leu Glu Ser His Leu Asp Asp Ala Glu Pro Tyr Leu Leu Thr Met Ala  
 225 230 235 240

Lys Lys Ala Leu Lys Ser Glu Ser Ala Ala Ser Ser Thr Gly Lys Glu  
 245 250 255

Asp Lys Gln Pro Ala Pro Gly Pro Val Glu Lys Pro Pro Arg Glu Pro  
 260 265 270

Ala Arg Gln Leu Arg Asn Pro Pro Thr Thr Ile Gly Met Met Thr Leu  
 275 280 285

Lys Ala Ala Phe Lys Thr Leu Ser Gly Ala Gln Asp Ser Glu Ala Ala  
 290 295 300

Phe Ala Lys Leu Asp Gln Lys Asp Leu Val Leu Pro Thr Gln Ala Leu  
 305 310 315 320

Pro Ala Ser Pro Ala Leu Lys Asn Lys Arg Pro Arg Lys Asp Glu Asn  
 325 330 335

Glu Ser Ser Ala Pro Ala Asp Gly Glu Gly Gly Ser Glu Leu Gln Pro  
 340 345 350

Lys Asn Lys Arg Met Thr Ile Ser Arg Leu Val Leu Glu Glu Asp Ser  
 355 360 365

Gln Ser Thr Glu Pro Ser Ala Gly Leu Asn Ser Ser Gln Glu Ala Ala  
 370 375 380

Ser Ala Pro Pro Ser Lys Pro Thr Val Leu Asn Gln Pro Leu Pro Gly  
 385 390 395 400

Glu Lys Asn Pro Lys Val Pro Lys Gly Lys Trp Asn Ser Ser Asn Gly  
 405 410 415

Val Glu Glu Lys Glu Thr Trp Val Glu Glu Asp Glu Leu Phe Gln Val  
 420 425 430

Gln Ala Ala Pro Asp Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln  
 435 440 445

Lys Trp Thr Val Glu Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys  
 450 455 460

Tyr Gly Glu Gly Asn Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val  
 465 470 475 480

Asn Arg Thr Ala Val Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg  
 485 490 495

Leu Gly Met Asn  
 500

<210> 2  
 <211> 543  
 <212> PRT  
 <213> Human

<400> 2

Met Ser Arg Glu Ser Asp Val Glu Ala Gln Gln Ser His Gly Ser Ser  
 1 5 10 15

Ala Cys Ser Gln Pro His Gly Ser Val Thr Gln Ser Gln Gly Ser Ser  
 20 25 30

Ser Gln Ser Gln Gly Ile Ser Ser Ser Ser Thr Ser Thr Met Pro Asn  
 35 40 45

Ser Ser Gln Ser Ser His Ser Ser Ser Gly Thr Leu Ser Ser Leu Glu  
 50 55 60

Thr Val Ser Thr Gln Glu Leu Tyr Ser Ile Pro Glu Asp Gln Glu Pro  
 65 70 75 80

Glu Asp Gln Glu Pro Glu Glu Pro Thr Pro Ala Pro Trp Ala Arg Leu  
 85 90 95

Trp Ala Leu Gln Asp Gly Phe Ala Asn Leu Glu Cys Val Asn Asp Asn  
100 105 110

Tyr Trp Phe Gly Arg Asp Lys Ser Cys Glu Tyr Cys Phe Asp Glu Pro  
115 120 125

Leu Leu Lys Arg Thr Asp Lys Tyr Arg Thr Tyr Ser Lys Lys His Phe  
130 135 140

Arg Ile Phe Arg Glu Val Gly Pro Lys Asn Ser Tyr Ile Ala Tyr Ile  
145 150 155 160

Glu Asp His Ser Gly Asn Gly Thr Phe Val Asn Thr Glu Leu Val Gly  
165 170 175

Lys Gly Lys Arg Arg Pro Leu Asn Asn Asn Ser Glu Ile Ala Leu Ser  
180 185 190

Leu Ser Arg Asn Lys Val Phe Val Phe Phe Asp Leu Thr Val Asp Asp  
195 200 205

Gln Ser Val Tyr Pro Lys Ala Leu Arg Asp Glu Tyr Ile Met Ser Lys  
210 215 220

Thr Leu Gly Ser Gly Ala Cys Gly Glu Val Lys Leu Ala Phe Glu Arg  
225 230 235 240

Lys Thr Cys Lys Lys Val Ala Ile Lys Ile Ile Ser Lys Arg Lys Phe  
245 250 255

Ala Ile Gly Ser Ala Arg Glu Ala Asp Pro Ala Leu Asn Val Glu Thr  
260 265 270

Glu Ile Glu Ile Leu Lys Lys Leu Asn His Pro Cys Ile Ile Lys Ile  
275 280 285

Lys Asn Phe Phe Asp Ala Glu Asp Tyr Tyr Ile Val Leu Glu Leu Met  
290 295 300

Glu Gly Gly Glu Leu Phe Asp Lys Val Val Gly Asn Lys Arg Leu Lys  
305 310 315 320

Glu Ala Thr Cys Lys Leu Tyr Phe Tyr Gln Met Leu Leu Ala Val Gln  
325 330 335

Tyr Leu His Glu Asn Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn  
 340 345 350

Val Leu Leu Ser Ser Gln Glu Glu Asp Cys Leu Ile Lys Ile Thr Asp  
 355 360 365

Phe Gly His Ser Lys Ile Leu Gly Glu Thr Ser Leu Met Arg Thr Leu  
 370 375 380

Cys Gly Thr Pro Thr Tyr Leu Ala Pro Glu Val Leu Val Ser Val Gly  
 385 390 395 400

Thr Ala Gly Tyr Asn Arg Ala Val Asp Cys Trp Ser Leu Gly Val Ile  
 405 410 415

Leu Phe Ile Cys Leu Ser Gly Tyr Pro Pro Phe Ser Glu His Arg Thr  
 420 425 430

Gln Val Ser Leu Lys Asp Gln Ile Thr Ser Gly Lys Tyr Asn Phe Ile  
 435 440 445

Pro Glu Val Trp Ala Glu Val Ser Glu Lys Ala Leu Asp Leu Val Lys  
 450 455 460

Lys Leu Leu Val Val Asp Pro Lys Ala Arg Phe Thr Thr Glu Glu Ala  
 465 470 475 480

Leu Arg His Pro Trp Leu Gln Asp Glu Asp Met Lys Arg Lys Phe Gln  
 485 490 495

Asp Leu Leu Ser Glu Glu Asn Glu Ser Thr Ala Leu Pro Gln Val Leu  
 500 505 510

Ala Gln Pro Ser Thr Ser Arg Lys Arg Pro Arg Glu Gly Glu Ala Glu  
 515 520 525

Gly Ala Glu Thr Thr Lys Arg Pro Ala Val Cys Ala Ala Val Leu  
 530 535 540

<210> 3  
 <211> 514  
 <212> PRT  
 <213> Human

<400> 3

Met Ser Arg Glu Ser Asp Val Glu Ala Gln Gln Ser His Gly Ser Ser

1	5	10	15
Ala Cys Ser Gln Pro His Gly Ser Val Thr Gln Ser Gln Gly Ser Ser	20	25	30
Ser Gln Ser Gln Gly Ile Ser Ser Ser Ser Thr Ser Thr Met Pro Asn	35	40	45
Ser Ser Gln Ser Ser His Ser Ser Ser Gly Thr Leu Ser Ser Leu Glu	50	55	60
Thr Val Ser Thr Gln Glu Leu Tyr Ser Ile Pro Glu Asp Gln Glu Pro	65	70	75
Glu Asp Gln Glu Pro Glu Glu Pro Thr Pro Ala Pro Trp Ala Arg Leu	85	90	95
Trp Ala Leu Gln Asp Gly Phe Ala Asn Leu Glu Cys Val Asn Asp Asn	100	105	110
Tyr Trp Phe Gly Arg Asp Lys Ser Cys Glu Tyr Cys Phe Asp Glu Pro	115	120	125
Leu Leu Lys Arg Thr Asp Lys Tyr Arg Thr Tyr Ser Lys Lys His Phe	130	135	140
Arg Ile Phe Arg Glu Val Gly Pro Lys Asn Ser Tyr Ile Ala Tyr Ile	145	150	155
Glu Asp His Ser Gly Asn Gly Thr Phe Val Asn Thr Glu Leu Val Gly	165	170	175
Lys Gly Lys Arg Arg Pro Leu Asn Asn Asn Ser Glu Ile Ala Leu Ser	180	185	190
Leu Ser Arg Asn Lys Val Phe Val Phe Phe Asp Leu Thr Val Asp Asp	195	200	205
Gln Ser Val Tyr Pro Lys Ala Leu Arg Asp Glu Tyr Ile Met Ser Lys	210	215	220
Thr Leu Gly Ser Gly Ala Cys Gly Glu Val Lys Leu Ala Phe Glu Arg	225	230	235
Lys Thr Cys Lys Lys Val Ala Ile Lys Ile Ile Ser Lys Arg Lys Phe	245	250	255

Ala Ile Gly Ser Ala Arg Glu Ala Asp Pro Ala Leu Asn Val Glu Thr  
 260 265 270

Glu Ile Glu Ile Leu Lys Lys Leu Asn His Pro Cys Ile Ile Lys Ile  
 275 280 285

Lys Asn Phe Phe Asp Ala Glu Asp Tyr Tyr Ile Val Leu Glu Leu Met  
 290 295 300

Glu Gly Gly Glu Leu Phe Asp Lys Val Val Gly Asn Lys Arg Leu Lys  
 305 310 315 320

Glu Ala Thr Cys Lys Leu Tyr Phe Tyr Gln Met Leu Leu Ala Val Gln  
 325 330 335

Ile Thr Asp Phe Gly His Ser Lys Ile Leu Gly Glu Thr Ser Leu Met  
 340 345 350

Arg Thr Leu Cys Gly Thr Pro Thr Tyr Leu Ala Pro Glu Val Leu Val  
 355 360 365

Ser Val Gly Thr Ala Gly Tyr Asn Arg Ala Val Asp Cys Trp Ser Leu  
 370 375 380

Gly Val Ile Leu Phe Ile Cys Leu Ser Gly Tyr Pro Pro Phe Ser Glu  
 385 390 395 400

His Arg Thr Gln Val Ser Leu Lys Asp Gln Ile Thr Ser Gly Lys Tyr  
 405 410 415

Asn Phe Ile Pro Glu Val Trp Ala Glu Val Ser Glu Lys Ala Leu Asp  
 420 425 430

Leu Val Lys Lys Leu Leu Val Val Asp Pro Lys Ala Arg Phe Thr Thr  
 435 440 445

Glu Glu Ala Leu Arg His Pro Trp Leu Gln Asp Glu Asp Met Lys Arg  
 450 455 460

Lys Phe Gln Asp Leu Leu Ser Glu Glu Asn Glu Ser Thr Ala Leu Pro  
 465 470 475 480

Gln Val Leu Ala Gln Pro Ser Thr Ser Arg Lys Arg Pro Arg Glu Gly  
 485 490 495

Glu Ala Glu Gly Ala Glu Thr Thr Lys Arg Pro Ala Val Cys Ala Ala  
 500 505 510

Val Leu

<210> 4  
 <211> 1233  
 <212> PRT  
 <213> human

<400> 4

Met Ala Asn Asp Ser Pro Ala Lys Ser Leu Val Asp Ile Asp Leu Ser  
 1 5 10 15

Ser Leu Arg Asp Pro Ala Gly Ile Phe Glu Leu Val Glu Val Val Gly  
 20 25 30

Asn Gly Thr Tyr Gly Gln Val Tyr Lys Gly Arg His Val Lys Thr Val  
 35 40 45

Thr Ala Ala Ile Lys Val Met Asp Val Thr Glu Asp Glu Glu Glu Glu  
 50 55 60

Ile Thr Leu Glu Ile Asn Met Leu Lys Lys Tyr Ser His His Arg Asn  
 65 70 75 80

Ile Ala Thr Tyr Tyr Gly Ala Phe Ile Lys Lys Ser Pro Pro Gly His  
 85 90 95

Asp Asp Gln Leu Trp Leu Val Met Glu Phe Cys Gly Ala Gly Ser Ile  
 100 105 110

Thr Asp Leu Val Lys Asn Thr Lys Gly Asn Thr Leu Lys Glu Asp Trp  
 115 120 125

Ile Ala Tyr Ile Ser Arg Glu Ile Leu Arg Gly Leu Ala His Leu His  
 130 135 140

Ile His His Val Ile His Arg Asp Ile Lys Gly Gln Asn Val Leu Leu  
 145 150 155 160

Thr Glu Asn Ala Glu Val Lys Leu Val Asp Phe Gly Val Ser Ala Gln  
 165 170 175

Leu Asp Arg Thr Val Gly Arg Arg Asn Thr Phe Ile Gly Thr Pro Tyr



180	185	190
Trp Met Ala Pro Glu Val Ile Ala Cys Asp Glu Asn Pro Asp Ala Thr		
195	200	205
Tyr Asp Tyr Arg Ser Asp Leu Trp Ser Cys Gly Ile Thr Ala Ile Glu		
210	215	220
Met Ala Glu Gly Gly Pro Pro Leu Cys Asp Met His Pro Met Arg Ala		
225	230	235 240
Leu Phe Leu Ile Pro Arg Asn Pro Pro Pro Arg Leu Lys Ser Lys Lys		
	245	250 255
Trp Ser Lys Lys Phe Phe Ser Phe Ile Glu Gly Cys Leu Val Lys Asn		
	260	265 270
Tyr Met Gln Arg Pro Ser Thr Glu Gln Leu Leu Lys His Pro Phe Ile		
	275	280 285
Arg Asp Gln Pro Asn Glu Arg Gln Val Arg Ile Gln Leu Lys Asp His		
	290	295 300
Ile Asp Arg Thr Arg Lys Lys Arg Gly Glu Lys Asp Glu Thr Glu Tyr		
305	310	315 320
Glu Tyr Ser Gly Ser Glu Glu Glu Glu Glu Glu Val Pro Glu Gln Glu		
	325	330 335
Gly Glu Pro Ser Ser Ile Val Asn Val Pro Gly Glu Ser Thr Leu Arg		
	340	345 350
Arg Asp Phe Leu Arg Leu Gln Gln Glu Asn Lys Glu Arg Ser Glu Ala		
	355	360 365
Leu Arg Arg Gln Gln Leu Leu Gln Glu Gln Gln Leu Arg Glu Gln Glu		
	370	375 380
Glu Tyr Lys Arg Gln Leu Leu Ala Glu Arg Gln Lys Arg Ile Glu Gln		
385	390	395 400
Gln Lys Glu Gln Arg Arg Arg Leu Glu Glu Gln Gln Arg Arg Glu Arg		
	405	410 415
Glu Ala Arg Arg Gln Gln Glu Arg Glu Gln Arg Arg Arg Glu Gln Glu		
	420	425 430

Glu Lys Arg Arg Leu Glu Glu Leu Glu Arg Arg Arg Lys Glu Glu Glu  
 435 440 445

Glu Arg Arg Arg Ala Glu Glu Glu Lys Arg Arg Val Glu Arg Glu Gln  
 450 455 460

Glu Tyr Ile Arg Arg Gln Leu Glu Glu Glu Gln Arg His Leu Glu Ile  
 465 470 475 480

Leu Gln Gln Gln Leu Leu Gln Glu Gln Ala Met Leu Leu His Asp His  
 485 490 495

Arg Arg Pro His Ala Gln Gln Gln Pro Pro Pro Pro Gln Gln Gln Asp  
 500 505 510

Arg Ser Lys Pro Ser Phe His Ala Pro Glu Pro Lys Pro His Tyr Asp  
 515 520 525

Pro Ala Asp Arg Ala Arg Glu Val Gln Trp Ser His Leu Ala Ser Leu  
 530 535 540

Lys Asn Asn Val Ser Pro Val Ser Arg Ser His Ser Phe Ser Asp Pro  
 545 550 555 560

Ser Pro Lys Phe Ala His His His Leu Arg Ser Gln Asp Pro Cys Pro  
 565 570 575

Pro Ser Arg Ser Glu Gly Leu Ser Gln Ser Ser Asp Ser Lys Ser Glu  
 580 585 590

Val Pro Glu Pro Thr Gln Lys Ala Trp Ser Arg Ser Asp Ser Asp Glu  
 595 600 605

Val Pro Pro Arg Val Pro Val Arg Thr Thr Ser Arg Ser Pro Val Leu  
 610 615 620

Ser Arg Arg Asp Ser Pro Leu Gln Gly Gly Gly Gln Gln Asn Ser Gln  
 625 630 635 640

Ala Gly Gln Arg Asn Ser Thr Ser Ser Ile Glu Pro Arg Leu Leu Trp  
 645 650 655

Glu Arg Val Glu Lys Leu Val Pro Arg Pro Gly Ser Gly Ser Ser Ser  
 660 665 670

Gly Ser Ser Asn Ser Gly Ser Gln Pro Gly Ser His Pro Gly Ser Gln  
 675 680 685

Ser Gly Ser Gly Glu Arg Phe Arg Val Arg Ser Ser Ser Lys Ser Glu  
 690 695 700

Gly Ser Pro Ser Pro Arg Gln Glu Ser Ala Ala Lys Lys Pro Asp Asp  
 705 710 715 720

Lys Lys Glu Val Phe Arg Ser Leu Lys Pro Ala Gly Glu Val Asp Leu  
 725 730 735

Thr Ala Leu Ala Lys Glu Leu Arg Ala Val Glu Asp Val Arg Pro Pro  
 740 745 750

His Lys Val Thr Asp Tyr Ser Ser Ser Ser Glu Glu Ser Gly Thr Thr  
 755 760 765

Asp Glu Glu Glu Glu Asp Val Glu Gln Glu Gly Ala Asp Asp Ser Thr  
 770 775 780

Ser Gly Pro Glu Asp Thr Arg Ala Ala Ser Ser Pro Asn Leu Ser Asn  
 785 790 795 800

Gly Glu Thr Glu Ser Val Lys Thr Met Ile Val His Asp Asp Val Glu  
 805 810 815

Ser Glu Pro Ala Met Thr Pro Ser Lys Glu Gly Thr Leu Ile Val Arg  
 820 825 830

Gln Thr Gln Ser Ala Ser Ser Thr Leu Gln Lys His Lys Ser Ser Ser  
 835 840 845

Ser Phe Thr Pro Phe Ile Asp Pro Arg Leu Leu Gln Ile Ser Pro Ser  
 850 855 860

Ser Gly Thr Thr Val Thr Ser Val Val Gly Phe Ser Cys Asp Gly Leu  
 865 870 875 880

Arg Pro Glu Ala Ile Arg Gln Asp Pro Thr Arg Lys Gly Ser Val Val  
 885 890 895

Asn Val Asn Pro Thr Asn Thr Arg Pro Gln Ser Asp Thr Pro Glu Ile  
 900 905 910

Arg Lys Tyr Lys Lys Arg Phe Asn Ser Glu Ile Leu Cys Ala Ala Leu  
 915 920 925

Trp Gly Val Asn Leu Leu Val Gly Thr Glu Ser Gly Leu Met Leu Leu  
 930 935 940

Asp Arg Ser Gly Gln Gly Lys Val Tyr Pro Leu Ile Ser Arg Arg Arg  
 945 950 955 960

Phe Gln Gln Met Asp Val Leu Glu Gly Leu Asn Val Leu Val Thr Ile  
 965 970 975

Ser Gly Lys Lys Asp Lys Leu Arg Val Tyr Tyr Leu Ser Trp Leu Arg  
 980 985 990

Asn Lys Ile Leu His Asn Asp Pro Glu Val Glu Lys Lys Gln Gly Trp  
 995 1000 1005

Thr Thr Val Gly Asp Leu Glu Gly Cys Val His Tyr Lys Val Val  
 1010 1015 1020

Lys Tyr Glu Arg Ile Lys Phe Leu Val Ile Ala Leu Lys Ser Ser  
 1025 1030 1035

Val Glu Val Tyr Ala Trp Ala Pro Lys Pro Tyr His Lys Phe Met  
 1040 1045 1050

Ala Phe Lys Ser Phe Gly Glu Leu Leu His Lys Pro Leu Leu Val  
 1055 1060 1065

Asp Leu Thr Val Glu Glu Gly Gln Arg Leu Lys Val Ile Tyr Gly  
 1070 1075 1080

Ser Cys Ala Gly Phe His Ala Val Asp Val Asp Ser Gly Ser Val  
 1085 1090 1095

Tyr Asp Ile Tyr Leu Pro Thr His Ile Gln Cys Ser Ile Lys Pro  
 1100 1105 1110

His Ala Ile Ile Ile Leu Pro Asn Thr Asp Gly Met Glu Leu Leu  
 1115 1120 1125

Val Cys Tyr Glu Asp Glu Gly Val Tyr Val Asn Thr Tyr Gly Arg  
 1130 1135 1140

Ile Thr Lys Asp Val Val Leu Gln Trp Gly Glu Met Pro Thr Ser

1145                      1150                      1155  
 Val Ala Tyr Ile Arg Ser Asn Gln Thr Met Gly Trp Gly Glu Lys  
 1160                      1165                      1170  
 Ala Ile Glu Ile Arg Ser Val Glu Thr Gly His Leu Asp Gly Val  
 1175                      1180                      1185  
 Phe Met His Lys Arg Ala Gln Arg Leu Lys Phe Leu Cys Gly Arg  
 1190                      1195                      1200  
 Asn Asp Lys Val Phe Phe Ser Ser Val Arg Ser Gly Gly Ser Ser  
 1205                      1210                      1215  
 Gln Val Tyr Phe Met Thr Leu Gly Arg Thr Ser Leu Leu Ser Trp  
 1220                      1225                      1230  
  
 <210> 5  
 <211> 1239  
 <212> PRT  
 <213> HUMAN  
  
 <400> 5  
 Met Ala Asn Asp Ser Pro Ala Lys Ser Leu Val Asp Ile Asp Leu Ser  
 1                      5                      10                      15  
 Ser Leu Arg Asp Pro Ala Gly Ile Phe Glu Leu Val Glu Val Val Gly  
 20                      25                      30  
 Asn Gly Thr Tyr Gly Gln Val Tyr Lys Gly Arg His Val Lys Thr Gly  
 35                      40                      45  
 Gln Leu Ala Ala Ile Lys Val Met Asp Val Thr Glu Asp Glu Glu Glu  
 50                      55                      60  
 Glu Ile Lys Leu Glu Ile Asn Met Leu Lys Lys Tyr Ser His His Arg  
 65                      70                      75                      80  
 Asn Ile Ala Thr Tyr Tyr Gly Ala Phe Ile Lys Lys Ser Pro Pro Gly  
 85                      90                      95  
 His Asp Asp Gln Leu Trp Leu Val Met Glu Phe Cys Gly Ala Gly Ser  
 100                      105                      110  
 Ile Thr Asp Leu Val Lys Asn Thr Lys Gly Asn Thr Leu Lys Glu Asp  
 115                      120                      125

Trp Ile Ala Tyr Ile Ser Arg Glu Ile Leu Arg Gly Leu Ala His Leu  
 130 135 140  
 His Ile His His Val Ile His Arg Asp Ile Lys Gly Gln Asn Val Leu  
 145 150 155 160  
 Leu Thr Glu Asn Ala Glu Val Lys Leu Val Asp Phe Gly Val Ser Ala  
 165 170 175  
 Gln Leu Asp Arg Thr Val Gly Arg Arg Asn Thr Phe Ile Gly Thr Pro  
 180 185 190  
 Tyr Trp Met Ala Pro Glu Val Ile Ala Cys Asp Glu Asn Pro Asp Ala  
 195 200 205  
 Thr Tyr Asp Tyr Arg Ser Asp Leu Trp Ser Cys Gly Ile Thr Ala Ile  
 210 215 220  
 Glu Met Ala Glu Gly Ala Pro Pro Leu Cys Asp Met His Pro Met Arg  
 225 230 235 240  
 Ala Leu Phe Leu Ile Pro Arg Asn Pro Pro Pro Arg Leu Lys Ser Lys  
 245 250 255  
 Lys Trp Ser Lys Lys Phe Phe Ser Phe Ile Glu Gly Cys Leu Val Lys  
 260 265 270  
 Asn Tyr Met Gln Arg Pro Ser Thr Glu Gln Leu Leu Lys His Pro Phe  
 275 280 285  
 Ile Arg Asp Gln Pro Asn Glu Arg Gln Val Arg Ile Gln Leu Lys Asp  
 290 295 300  
 His Ile Asp Arg Thr Arg Lys Lys Arg Gly Glu Lys Asp Glu Thr Glu  
 305 310 315 320  
 Tyr Glu Tyr Ser Gly Ser Glu Glu Glu Glu Glu Glu Val Pro Glu Gln  
 325 330 335  
 Glu Gly Glu Pro Ser Ser Ile Val Asn Val Pro Gly Glu Ser Thr Leu  
 340 345 350  
 Arg Arg Asp Phe Leu Arg Leu Gln Gln Glu Asn Lys Glu Arg Ser Glu  
 355 360 365

Ala Leu Arg Arg Gln Gln Leu Leu Gln Glu Gln Gln Leu Arg Glu Gln  
 370 375 380

Glu Glu Tyr Lys Arg Gln Leu Leu Ala Glu Arg Gln Lys Arg Ile Glu  
 385 390 395 400

Gln Gln Lys Glu Gln Arg Arg Arg Leu Glu Glu Gln Gln Arg Arg Glu  
 405 410 415

Arg Glu Ala Arg Arg Gln Gln Glu Arg Glu Gln Arg Arg Arg Glu Gln  
 420 425 430

Glu Glu Lys Arg Arg Leu Glu Glu Leu Glu Arg Arg Arg Lys Glu Glu  
 435 440 445

Glu Glu Arg Arg Arg Ala Glu Glu Glu Lys Arg Arg Val Glu Arg Glu  
 450 455 460

Gln Glu Tyr Ile Arg Arg Gln Leu Glu Glu Glu Gln Arg His Leu Glu  
 465 470 475 480

Val Leu Gln Gln Gln Leu Leu Gln Glu Gln Ala Met Leu Leu Glu Cys  
 485 490 495

Arg Trp Arg Glu Met Glu Glu His Arg Gln Ala Glu Arg Leu Gln Arg  
 500 505 510

Gln Leu Gln Gln Glu Gln Ala Tyr Leu Leu Ser Leu Gln His Asp His  
 515 520 525

Arg Arg Pro His Pro Gln His Ser Gln Gln Pro Pro Pro Pro Gln Gln  
 530 535 540

Glu Arg Ser Lys Pro Ser Phe His Ala Pro Glu Pro Lys Ala His Tyr  
 545 550 555 560

Glu Pro Ala Asp Arg Ala Arg Glu Val Glu Asp Arg Phe Arg Lys Thr  
 565 570 575

Asn His Ser Ser Pro Glu Ala Gln Ser Lys Gln Thr Gly Arg Val Leu  
 580 585 590

Glu Pro Pro Val Pro Ser Arg Ser Glu Ser Phe Ser Asn Gly Asn Ser  
 595 600 605

Glu Ser Val His Pro Ala Leu Gln Arg Pro Ala Glu Pro Gln Val Pro

610		615		620
Val Arg Thr Thr Ser Arg Ser Pro Val Leu Ser Arg Arg Asp Ser Pro				
625		630		635 640
Leu Gln Gly Ser Gly Gln Gln Asn Ser Gln Ala Gly Gln Arg Asn Ser				
	645		650	655
Thr Ser Ile Glu Pro Arg Leu Leu Trp Glu Arg Val Glu Lys Leu Val				
	660		665	670
Pro Arg Pro Gly Ser Gly Ser Ser Ser Gly Ser Ser Asn Ser Gly Ser				
	675		680	685
Gln Pro Gly Ser His Pro Gly Ser Gln Ser Gly Ser Gly Glu Arg Phe				
	690		695	700
Arg Val Arg Ser Ser Ser Lys Ser Glu Gly Ser Pro Ser Gln Arg Leu				
705		710	715	720
Glu Asn Ala Val Lys Lys Pro Glu Asp Lys Lys Glu Val Phe Arg Pro				
	725		730	735
Leu Lys Pro Ala Asp Leu Thr Ala Leu Ala Lys Glu Leu Arg Ala Val				
	740		745	750
Glu Asp Val Arg Pro Pro His Lys Val Thr Asp Tyr Ser Ser Ser Ser				
	755		760	765
Glu Glu Ser Gly Thr Thr Asp Glu Glu Asp Asp Asp Val Glu Gln Glu				
	770		775	780
Gly Ala Asp Glu Ser Thr Ser Gly Pro Glu Asp Thr Arg Ala Ala Ser				
785		790	795	800
Ser Leu Asn Leu Ser Asn Gly Glu Thr Glu Ser Val Lys Thr Met Ile				
	805		810	815
Val His Asp Asp Val Glu Ser Glu Pro Ala Met Thr Pro Ser Lys Glu				
	820		825	830
Gly Thr Leu Ile Val Arg Gln Thr Gln Ser Ala Ser Ser Thr Leu Gln				
	835		840	845
Lys His Lys Ser Ser Ser Ser Phe Thr Pro Phe Ile Asp Pro Arg Leu				
	850		855	860



Leu Gln Ile Ser Pro Ser Ser Gly Thr Thr Val Thr Ser Val Val Gly  
865 870 875 880

Phe Ser Cys Asp Gly Met Arg Pro Glu Ala Ile Arg Gln Asp Pro Thr  
885 890 895

Arg Lys Gly Ser Val Val Asn Val Asn Pro Thr Asn Thr Arg Pro Gln  
900 905 910

Ser Asp Thr Pro Glu Ile Arg Lys Tyr Lys Lys Arg Phe Asn Ser Glu  
915 920 925

Ile Leu Cys Ala Ala Leu Trp Gly Val Asn Leu Leu Val Gly Thr Glu  
930 935 940

Ser Gly Leu Met Leu Leu Asp Arg Ser Gly Gln Gly Lys Val Tyr Pro  
945 950 955 960

Leu Ile Asn Arg Arg Arg Phe Gln Gln Met Asp Val Leu Glu Gly Leu  
965 970 975

Asn Val Leu Val Thr Ile Ser Gly Lys Lys Asp Lys Leu Arg Val Tyr  
980 985 990

Tyr Leu Ser Trp Leu Arg Asn Lys Ile Leu His Asn Asp Pro Glu Val  
995 1000 1005

Glu Lys Lys Gln Gly Trp Thr Thr Val Gly Asp Leu Glu Gly Cys  
1010 1015 1020

Val His Tyr Lys Val Val Lys Tyr Glu Arg Ile Lys Phe Leu Val  
1025 1030 1035

Ile Ala Leu Lys Ser Ser Val Glu Val Tyr Ala Trp Ala Pro Lys  
1040 1045 1050

Pro Tyr His Lys Phe Met Ala Phe Lys Ser Phe Gly Glu Leu Val  
1055 1060 1065

His Lys Pro Leu Leu Val Asp Leu Thr Val Glu Glu Gly Gln Arg  
1070 1075 1080

Leu Lys Val Ile Tyr Gly Ser Cys Ala Gly Phe His Ala Val Asp  
1085 1090 1095

Val Asp Ser Gly Ser Val Tyr Asp Ile Tyr Leu Pro Thr His Ile  
 1100 1105 1110

Gln Cys Ser Ile Lys Pro His Ala Ile Ile Ile Leu Pro Asn Thr  
 1115 1120 1125

Asp Gly Met Glu Leu Leu Val Cys Tyr Glu Asp Glu Gly Val Tyr  
 1130 1135 1140

Val Asn Thr Tyr Gly Arg Ile Thr Lys Asp Val Val Leu Gln Trp  
 1145 1150 1155

Gly Glu Met Pro Thr Ser Val Ala Tyr Ile Arg Ser Asn Gln Thr  
 1160 1165 1170

Met Gly Trp Gly Glu Lys Ala Ile Glu Ile Arg Ser Val Glu Thr  
 1175 1180 1185

Gly His Leu Asp Gly Val Phe Met His Lys Arg Ala Gln Arg Leu  
 1190 1195 1200

Lys Phe Leu Cys Glu Arg Asn Asp Lys Val Phe Phe Ala Ser Val  
 1205 1210 1215

Arg Ser Gly Gly Ser Ser Gln Val Tyr Phe Met Thr Leu Gly Arg  
 1220 1225 1230

Thr Ser Leu Leu Ser Trp  
 1235

<210> 6  
 <211> 1212  
 <212> PRT  
 <213> HUMAN

<400> 6

Met Ala Asn Asp Ser Pro Ala Lys Ser Leu Val Asp Ile Asp Leu Ser  
 1 5 10 15

Ser Leu Arg Asp Pro Ala Gly Ile Phe Glu Leu Val Glu Val Val Gly  
 20 25 30

Asn Gly Thr Tyr Gly Gln Val Tyr Lys Gly Arg His Val Lys Thr Gly  
 35 40 45

Gln Leu Ala Ala Ile Lys Val Met Asp Val Thr Glu Asp Glu Glu Glu

50		55		60
Glu Ile Lys Leu Glu Ile Asn Met Leu Lys Lys Tyr Ser His His Arg				
65		70		75
Asn Ile Ala Thr Tyr Tyr Gly Ala Phe Ile Lys Lys Ser Pro Pro Gly				
	85		90	95
His Asp Asp Gln Leu Trp Leu Val Met Glu Phe Cys Gly Ala Gly Ser				
	100		105	110
Ile Thr Asp Leu Val Lys Asn Thr Lys Gly Asn Thr Leu Lys Glu Asp				
	115		120	125
Trp Ile Ala Tyr Ile Ser Arg Glu Ile Leu Arg Gly Leu Ala His Leu				
	130		135	140
His Ile His His Val Ile His Arg Asp Ile Lys Gly Gln Asn Val Leu				
145		150		155
Leu Thr Glu Asn Ala Glu Val Lys Leu Val Asp Phe Gly Val Ser Ala				
	165		170	175
Gln Leu Asp Arg Thr Val Gly Arg Arg Asn Thr Phe Ile Gly Thr Pro				
	180		185	190
Tyr Trp Met Ala Pro Glu Val Ile Ala Cys Asp Glu Asn Pro Asp Ala				
	195		200	205
Thr Tyr Asp Tyr Arg Ser Asp Leu Trp Ser Cys Gly Ile Thr Ala Ile				
	210		215	220
Glu Met Ala Glu Gly Ala Pro Pro Leu Cys Asp Met His Pro Met Arg				
225		230		235
Ala Leu Phe Leu Ile Pro Arg Asn Pro Pro Pro Arg Leu Lys Ser Lys				
	245		250	255
Lys Trp Ser Lys Lys Phe Phe Ser Phe Ile Glu Gly Cys Leu Val Lys				
	260		265	270
Asn Tyr Met Gln Arg Pro Ser Thr Glu Gln Leu Leu Lys His Pro Phe				
	275		280	285
Ile Arg Asp Gln Pro Asn Glu Arg Gln Val Arg Ile Gln Leu Lys Asp				
	290		295	300

His Ile Asp Arg Thr Arg Lys Lys Arg Gly Glu Lys Asp Glu Thr Glu  
 305 310 315 320

Tyr Glu Tyr Ser Gly Ser Glu Glu Glu Glu Glu Glu Val Pro Glu Gln  
 325 330 335

Glu Gly Glu Pro Ser Ser Ile Val Asn Val Pro Gly Glu Ser Thr Leu  
 340 345 350

Arg Arg Asp Phe Leu Arg Leu Gln Gln Glu Asn Lys Glu Arg Ser Glu  
 355 360 365

Ala Leu Arg Arg Gln Gln Leu Leu Gln Glu Gln Gln Leu Arg Glu Gln  
 370 375 380

Glu Glu Tyr Lys Arg Gln Leu Leu Ala Glu Arg Gln Lys Arg Ile Glu  
 385 390 395 400

Gln Gln Lys Glu Gln Arg Arg Arg Leu Glu Glu Gln Gln Arg Arg Glu  
 405 410 415

Arg Glu Ala Arg Arg Gln Gln Glu Arg Glu Gln Arg Arg Arg Glu Gln  
 420 425 430

Glu Glu Lys Arg Arg Leu Glu Glu Leu Glu Arg Arg Arg Lys Glu Glu  
 435 440 445

Glu Glu Arg Arg Arg Ala Glu Glu Glu Lys Arg Arg Val Glu Arg Glu  
 450 455 460

Gln Glu Tyr Ile Arg Arg Gln Leu Glu Glu Glu Gln Arg His Leu Glu  
 465 470 475 480

Val Leu Gln Gln Gln Leu Leu Gln Glu Gln Ala Met Leu Leu His Asp  
 485 490 495

His Arg Arg Pro His Pro Gln His Ser Gln Gln Pro Pro Pro Pro Gln  
 500 505 510

Gln Glu Arg Ser Lys Pro Ser Phe His Ala Pro Glu Pro Lys Ala His  
 515 520 525

Tyr Glu Pro Ala Asp Arg Ala Arg Glu Val Glu Asp Arg Phe Arg Lys  
 530 535 540

Thr Asn His Ser Ser Pro Glu Ala Gln Ser Lys Gln Thr Gly Arg Val  
 545 550 555 560

Leu Glu Pro Pro Val Pro Ser Arg Ser Glu Ser Phe Ser Asn Gly Asn  
 565 570 575

Ser Glu Ser Val His Pro Ala Leu Gln Arg Pro Ala Glu Pro Gln Val  
 580 585 590

Pro Val Arg Thr Thr Ser Arg Ser Pro Val Leu Ser Arg Arg Asp Ser  
 595 600 605

Pro Leu Gln Gly Ser Gly Gln Gln Asn Ser Gln Ala Gly Gln Arg Asn  
 610 615 620

Ser Thr Ser Ser Ile Glu Pro Arg Leu Leu Trp Glu Arg Val Glu Lys  
 625 630 635 640

Leu Val Pro Arg Pro Gly Ser Gly Ser Ser Ser Gly Ser Ser Asn Ser  
 645 650 655

Gly Ser Gln Pro Gly Ser His Pro Gly Ser Gln Ser Gly Ser Gly Glu  
 660 665 670

Arg Phe Arg Val Arg Ser Ser Ser Lys Ser Glu Gly Ser Pro Ser Gln  
 675 680 685

Arg Leu Glu Asn Ala Val Lys Lys Pro Glu Asp Lys Lys Glu Val Phe  
 690 695 700

Arg Pro Leu Lys Pro Ala Gly Glu Val Asp Leu Thr Ala Leu Ala Lys  
 705 710 715 720

Glu Leu Arg Ala Val Glu Asp Val Arg Pro Pro His Lys Val Thr Asp  
 725 730 735

Tyr Ser Ser Ser Ser Glu Glu Ser Gly Thr Thr Asp Glu Glu Asp Asp  
 740 745 750

Asp Val Glu Gln Glu Gly Ala Asp Glu Ser Thr Ser Gly Pro Glu Asp  
 755 760 765

Thr Arg Ala Ala Ser Ser Leu Asn Leu Ser Asn Gly Glu Thr Glu Ser  
 770 775 780

Val Lys Thr Met Ile Val His Asp Asp Val Glu Ser Glu Pro Ala Met  
 785 790 795 800

Thr Pro Ser Lys Glu Gly Thr Leu Ile Val Arg Gln Thr Gln Ser Ala  
 805 810 815

Ser Ser Thr Leu Gln Lys His Lys Ser Ser Ser Ser Phe Thr Pro Phe  
 820 825 830

Ile Asp Pro Arg Leu Leu Gln Ile Ser Pro Ser Ser Gly Thr Thr Val  
 835 840 845

Thr Ser Val Val Gly Phe Ser Cys Asp Gly Met Arg Pro Glu Ala Ile  
 850 855 860

Arg Gln Asp Pro Thr Arg Lys Gly Ser Val Val Asn Val Asn Pro Thr  
 865 870 875 880

Asn Thr Arg Pro Gln Ser Asp Thr Pro Glu Ile Arg Lys Tyr Lys Lys  
 885 890 895

Arg Phe Asn Ser Glu Ile Leu Cys Ala Ala Leu Trp Gly Val Asn Leu  
 900 905 910

Leu Val Gly Thr Glu Ser Gly Leu Met Leu Leu Asp Arg Ser Gly Gln  
 915 920 925

Gly Lys Val Tyr Pro Leu Ile Asn Arg Arg Arg Phe Gln Gln Met Asp  
 930 935 940

Val Leu Glu Gly Leu Asn Val Leu Val Thr Ile Ser Gly Lys Lys Asp  
 945 950 955 960

Lys Leu Arg Val Tyr Tyr Leu Ser Trp Leu Arg Asn Lys Ile Leu His  
 965 970 975

Asn Asp Pro Glu Val Glu Lys Lys Gln Gly Trp Thr Thr Val Gly Asp  
 980 985 990

Leu Glu Gly Cys Val His Tyr Lys Val Val Lys Tyr Glu Arg Ile Lys  
 995 1000 1005

Phe Leu Val Ile Ala Leu Lys Ser Ser Val Glu Val Tyr Ala Trp  
 1010 1015 1020

Ala Pro Lys Pro Tyr His Lys Phe Met Ala Phe Lys Ser Phe Gly

1025		1030		1035
Glu Leu Val His Lys Pro Leu	Leu Val Asp Leu Thr	Val Glu Glu		
1040	1045	1050		
Gly Gln Arg Leu Lys Val Ile	Tyr Gly Ser Cys Ala	Gly Phe His		
1055	1060	1065		
Ala Val Asp Val Asp Ser Gly	Ser Val Tyr Asp Ile	Tyr Leu Pro		
1070	1075	1080		
Thr His Ile Gln Cys Ser Ile	Lys Pro His Ala Ile	Ile Ile Leu		
1085	1090	1095		
Pro Asn Thr Asp Gly Met Glu	Leu Leu Val Cys Tyr	Glu Asp Glu		
1100	1105	1110		
Gly Val Tyr Val Asn Thr Tyr	Gly Arg Ile Thr Lys	Asp Val Val		
1115	1120	1125		
Leu Gln Trp Gly Glu Met Pro	Thr Ser Val Ala Tyr	Ile Arg Ser		
1130	1135	1140		
Asn Gln Thr Met Gly Trp Gly	Glu Lys Ala Ile Glu	Ile Arg Ser		
1145	1150	1155		
Val Glu Thr Gly His Leu Asp	Gly Val Phe Met His	Lys Arg Ala		
1160	1165	1170		
Gln Arg Leu Lys Phe Leu Cys	Glu Arg Asn Asp Lys	Val Phe Phe		
1175	1180	1185		
Ala Ser Val Arg Ser Gly Gly	Ser Ser Gln Val Tyr	Phe Met Thr		
1190	1195	1200		
Leu Gly Arg Thr Ser Leu Leu	Ser Trp			
1205	1210			

<210> 7  
 <211> 1320  
 <212> PRT  
 <213> HUMAN

<400> 7

Met	Ala	Asn	Asp	Ser	Pro	Ala	Lys	Ser	Leu	Val	Asp	Ile	Asp	Leu	Ser
1				5					10					15	

Ser Leu Arg Asp Pro Ala Gly Ile Phe Glu Leu Val Glu Val Val Gly  
 20 25 30

Asn Gly Thr Tyr Gly Gln Val Tyr Lys Gly Arg His Val Lys Thr Gly  
 35 40 45

Gln Leu Ala Ala Ile Lys Val Met Asp Val Thr Glu Asp Glu Glu Glu  
 50 55 60

Glu Ile Lys Leu Glu Ile Asn Met Leu Lys Lys Tyr Ser His His Arg  
 65 70 75 80

Asn Ile Ala Thr Tyr Tyr Gly Ala Phe Ile Lys Lys Ser Pro Pro Gly  
 85 90 95

His Asp Asp Gln Leu Trp Leu Val Met Glu Phe Cys Gly Ala Gly Ser  
 100 105 110

Ile Thr Asp Leu Val Lys Asn Thr Lys Gly Asn Thr Leu Lys Glu Asp  
 115 120 125

Trp Ile Ala Tyr Ile Ser Arg Glu Ile Leu Arg Gly Leu Ala His Leu  
 130 135 140

His Ile His His Val Ile His Arg Asp Ile Lys Gly Gln Asn Val Leu  
 145 150 155 160

Leu Thr Glu Asn Ala Glu Val Lys Leu Val Asp Phe Gly Val Ser Ala  
 165 170 175

Gln Leu Asp Arg Thr Val Gly Arg Arg Asn Thr Phe Ile Gly Thr Pro  
 180 185 190

Tyr Trp Met Ala Pro Glu Val Ile Ala Cys Asp Glu Asn Pro Asp Ala  
 195 200 205

Thr Tyr Asp Tyr Arg Ser Asp Leu Trp Ser Cys Gly Ile Thr Ala Ile  
 210 215 220

Glu Met Ala Glu Gly Ala Pro Pro Leu Cys Asp Met His Pro Met Arg  
 225 230 235 240

Ala Leu Phe Leu Ile Pro Arg Asn Pro Pro Pro Arg Leu Lys Ser Lys  
 245 250 255



Lys Trp Ser Lys Lys Phe Phe Ser Phe Ile Glu Gly Cys Leu Val Lys  
260 265 270

Asn Tyr Met Gln Arg Pro Ser Thr Glu Gln Leu Leu Lys His Pro Phe  
275 280 285

Ile Arg Asp Gln Pro Asn Glu Arg Gln Val Arg Ile Gln Leu Lys Asp  
290 295 300

His Ile Asp Arg Thr Arg Lys Lys Arg Gly Glu Lys Asp Glu Thr Glu  
305 310 315 320

Tyr Glu Tyr Ser Gly Ser Glu Glu Glu Glu Glu Glu Val Pro Glu Gln  
325 330 335

Glu Gly Glu Pro Ser Ser Ile Val Asn Val Pro Gly Glu Ser Thr Leu  
340 345 350

Arg Arg Asp Phe Leu Arg Leu Gln Gln Glu Asn Lys Glu Arg Ser Glu  
355 360 365

Ala Leu Arg Arg Gln Gln Leu Leu Gln Glu Gln Gln Leu Arg Glu Gln  
370 375 380

Glu Glu Tyr Lys Arg Gln Leu Leu Ala Glu Arg Gln Lys Arg Ile Glu  
385 390 395 400

Gln Gln Lys Glu Gln Arg Arg Arg Leu Glu Glu Gln Gln Arg Arg Glu  
405 410 415

Arg Glu Ala Arg Arg Gln Gln Glu Arg Glu Gln Arg Arg Arg Glu Gln  
420 425 430

Glu Glu Lys Arg Arg Leu Glu Glu Leu Glu Arg Arg Arg Lys Glu Glu  
435 440 445

Glu Glu Arg Arg Arg Ala Glu Glu Glu Lys Arg Arg Val Glu Arg Glu  
450 455 460

Gln Glu Tyr Ile Arg Arg Gln Leu Glu Glu Glu Gln Arg His Leu Glu  
465 470 475 480

Val Leu Gln Gln Gln Leu Leu Gln Glu Gln Ala Met Leu Leu Glu Cys  
485 490 495

Arg Trp Arg Glu Met Glu Glu His Arg Gln Ala Glu Arg Leu Gln Arg

500					505					510					
Gln	Leu	Gln	Gln	Glu	Gln	Ala	Tyr	Leu	Leu	Ser	Leu	Gln	His	Asp	His
	515						520					525			
Arg	Arg	Pro	His	Pro	Gln	His	Ser	Gln	Gln	Pro	Pro	Pro	Pro	Gln	Gln
	530					535					540				
Glu	Arg	Ser	Lys	Pro	Ser	Phe	His	Ala	Pro	Glu	Pro	Lys	Ala	His	Tyr
545					550					555					560
Glu	Pro	Ala	Asp	Arg	Ala	Arg	Glu	Val	Glu	Asp	Arg	Phe	Arg	Lys	Thr
				565					570					575	
Asn	His	Ser	Ser	Pro	Glu	Ala	Gln	Ser	Lys	Gln	Thr	Gly	Arg	Val	Leu
			580					585					590		
Glu	Pro	Pro	Val	Pro	Ser	Arg	Ser	Glu	Ser	Phe	Ser	Asn	Gly	Asn	Ser
		595					600					605			
Glu	Ser	Val	His	Pro	Ala	Leu	Gln	Arg	Pro	Ala	Glu	Pro	Gln	Val	Gln
610						615					620				
Trp	Ser	His	Leu	Ala	Ser	Leu	Lys	Asn	Asn	Val	Ser	Pro	Val	Ser	Arg
625					630					635					640
Ser	His	Ser	Phe	Ser	Asp	Pro	Ser	Pro	Lys	Phe	Ala	His	His	His	Leu
				645					650					655	
Arg	Ser	Gln	Asp	Pro	Cys	Pro	Pro	Ser	Arg	Ser	Glu	Val	Leu	Ser	Gln
			660					665					670		
Ser	Ser	Asp	Ser	Lys	Ser	Glu	Ala	Pro	Asp	Pro	Thr	Gln	Lys	Ala	Trp
		675					680					685			
Ser	Arg	Ser	Asp	Ser	Asp	Glu	Val	Pro	Pro	Arg	Val	Pro	Val	Arg	Thr
	690					695					700				
Thr	Ser	Arg	Ser	Pro	Val	Leu	Ser	Arg	Arg	Asp	Ser	Pro	Leu	Gln	Gly
705					710					715					720
Ser	Gly	Gln	Gln	Asn	Ser	Gln	Ala	Gly	Gln	Arg	Asn	Ser	Thr	Ser	Ser
				725					730					735	
Ile	Glu	Pro	Arg	Leu	Leu	Trp	Glu	Arg	Val	Glu	Lys	Leu	Val	Pro	Arg
			740					745					750		

Pro Gly Ser Gly Ser Ser Ser Gly Ser Ser Asn Ser Gly Ser Gln Pro  
755 760 765

Gly Ser His Pro Gly Ser Gln Ser Gly Ser Gly Glu Arg Phe Arg Val  
770 775 780

Arg Ser Ser Ser Lys Ser Glu Gly Ser Pro Ser Gln Arg Leu Glu Asn  
785 790 795 800

Ala Val Lys Lys Pro Glu Asp Lys Lys Glu Val Phe Arg Pro Leu Lys  
805 810 815

Pro Ala Gly Glu Val Asp Leu Thr Ala Leu Ala Lys Glu Leu Arg Ala  
820 825 830

Val Glu Asp Val Arg Pro Pro His Lys Val Thr Asp Tyr Ser Ser Ser  
835 840 845

Ser Glu Glu Ser Gly Thr Thr Asp Glu Glu Asp Asp Asp Val Glu Gln  
850 855 860

Glu Gly Ala Asp Glu Ser Thr Ser Gly Pro Glu Asp Thr Arg Ala Ala  
865 870 875 880

Ser Ser Leu Asn Leu Ser Asn Gly Glu Thr Glu Ser Val Lys Thr Met  
885 890 895

Ile Val His Asp Asp Val Glu Ser Glu Pro Ala Met Thr Pro Ser Lys  
900 905 910

Glu Gly Thr Leu Ile Val Arg Gln Thr Gln Ser Ala Ser Ser Thr Leu  
915 920 925

Gln Lys His Lys Ser Ser Ser Ser Phe Thr Pro Phe Ile Asp Pro Arg  
930 935 940

Leu Leu Gln Ile Ser Pro Ser Ser Gly Thr Thr Val Thr Ser Val Val  
945 950 955 960

Gly Phe Ser Cys Asp Gly Met Arg Pro Glu Ala Ile Arg Gln Asp Pro  
965 970 975

Thr Arg Lys Gly Ser Val Val Asn Val Asn Pro Thr Asn Thr Arg Pro  
980 985 990

Gln Ser Asp Thr Pro Glu Ile Arg Lys Tyr Lys Lys Arg Phe Asn Ser  
 995 1000 1005

Glu Ile Leu Cys Ala Ala Leu Trp Gly Val Asn Leu Leu Val Gly  
 1010 1015 1020

Thr Glu Ser Gly Leu Met Leu Leu Asp Arg Ser Gly Gln Gly Lys  
 1025 1030 1035

Val Tyr Pro Leu Ile Asn Arg Arg Arg Phe Gln Gln Met Asp Val  
 1040 1045 1050

Leu Glu Gly Leu Asn Val Leu Val Thr Ile Ser Gly Lys Lys Asp  
 1055 1060 1065

Lys Leu Arg Val Tyr Tyr Leu Ser Trp Leu Arg Asn Lys Ile Leu  
 1070 1075 1080

His Asn Asp Pro Glu Val Glu Lys Lys Gln Gly Trp Thr Thr Val  
 1085 1090 1095

Gly Asp Leu Glu Gly Cys Val His Tyr Lys Val Val Lys Tyr Glu  
 1100 1105 1110

Arg Ile Lys Phe Leu Val Ile Ala Leu Lys Ser Ser Val Glu Val  
 1115 1120 1125

Tyr Ala Trp Ala Pro Lys Pro Tyr His Lys Phe Met Ala Phe Lys  
 1130 1135 1140

Ser Phe Gly Glu Leu Val His Lys Pro Leu Leu Val Asp Leu Thr  
 1145 1150 1155

Val Glu Glu Gly Gln Arg Leu Lys Val Ile Tyr Gly Ser Cys Ala  
 1160 1165 1170

Gly Phe His Ala Val Asp Val Asp Ser Gly Ser Val Tyr Asp Ile  
 1175 1180 1185

Tyr Leu Pro Thr His Ile Gln Cys Ser Ile Lys Pro His Ala Ile  
 1190 1195 1200

Ile Ile Leu Pro Asn Thr Asp Gly Met Glu Leu Leu Val Cys Tyr  
 1205 1210 1215

Glu Asp Glu Gly Val Tyr Val Asn Thr Tyr Gly Arg Ile Thr Lys  
 1220 1225 1230

Asp Val Val Leu Gln Trp Gly Glu Met Pro Thr Ser Val Ala Tyr  
 1235 1240 1245

Ile Arg Ser Asn Gln Thr Met Gly Trp Gly Glu Lys Ala Ile Glu  
 1250 1255 1260

Ile Arg Ser Val Glu Thr Gly His Leu Asp Gly Val Phe Met His  
 1265 1270 1275

Lys Arg Ala Gln Arg Leu Lys Phe Leu Cys Glu Arg Asn Asp Lys  
 1280 1285 1290

Val Phe Phe Ala Ser Val Arg Ser Gly Gly Ser Ser Gln Val Tyr  
 1295 1300 1305

Phe Met Thr Leu Gly Arg Thr Ser Leu Leu Ser Trp  
 1310 1315 1320

<210> 8  
 <211> 1166  
 <212> PRT  
 <213> HUMAN

<400> 8

Met Ala Asn Asp Ser Pro Ala Lys Ser Leu Val Asp Ile Asp Leu Ser  
 1 5 10 15

Ser Leu Arg Asp Pro Ala Gly Ile Phe Glu Leu Val Glu Val Val Gly  
 20 25 30

Asn Gly Thr Tyr Gly Gln Val Tyr Lys Gly Arg His Val Lys Thr Gly  
 35 40 45

Gln Leu Ala Ala Ile Lys Val Met Asp Val Thr Glu Asp Glu Glu Glu  
 50 55 60

Glu Ile Lys Leu Glu Ile Asn Met Leu Lys Lys Tyr Ser His His Arg  
 65 70 75 80

Asn Ile Ala Thr Tyr Tyr Gly Ala Phe Ile Lys Lys Ser Pro Pro Gly  
 85 90 95

His Asp Asp Gln Leu Trp Leu Val Met Glu Phe Cys Gly Ala Gly Ser  
 100 105 110

Ile Thr Asp Leu Val Lys Asn Thr Lys Gly Asn Thr Leu Lys Glu Asp  
115 120 125

Trp Ile Ala Tyr Ile Ser Arg Glu Ile Leu Arg Gly Leu Ala His Leu  
130 135 140

His Ile His His Val Ile His Arg Asp Ile Lys Gly Gln Asn Val Leu  
145 150 155 160

Leu Thr Glu Asn Ala Glu Val Lys Leu Val Asp Phe Gly Val Ser Ala  
165 170 175

Gln Leu Asp Arg Thr Val Gly Arg Arg Asn Thr Phe Ile Gly Thr Pro  
180 185 190

Tyr Trp Met Ala Pro Glu Val Ile Ala Cys Asp Glu Asn Pro Asp Ala  
195 200 205

Thr Tyr Asp Tyr Arg Ser Asp Leu Trp Ser Cys Gly Ile Thr Ala Ile  
210 215 220

Glu Met Ala Glu Gly Ala Pro Pro Leu Cys Asp Met His Pro Met Arg  
225 230 235 240

Ala Leu Phe Leu Ile Pro Arg Asn Pro Pro Pro Arg Leu Lys Ser Lys  
245 250 255

Lys Trp Ser Lys Lys Phe Phe Ser Phe Ile Glu Gly Cys Leu Val Lys  
260 265 270

Asn Tyr Met Gln Arg Pro Ser Thr Glu Gln Leu Leu Lys His Pro Phe  
275 280 285

Ile Arg Asp Gln Pro Asn Glu Arg Gln Val Arg Ile Gln Leu Lys Asp  
290 295 300

His Ile Asp Arg Thr Arg Lys Lys Arg Gly Glu Lys Asp Glu Thr Glu  
305 310 315 320

Tyr Glu Tyr Ser Gly Ser Glu Glu Glu Glu Glu Glu Val Pro Glu Gln  
325 330 335

Glu Gly Glu Pro Ser Ser Ile Val Asn Val Pro Gly Glu Ser Thr Leu  
340 345 350

Arg Arg Asp Phe Leu Arg Leu Gln Gln Glu Asn Lys Glu Arg Ser Glu  
 355 360 365

Ala Leu Arg Arg Gln Gln Leu Leu Gln Glu Gln Gln Leu Arg Glu Gln  
 370 375 380

Glu Glu Tyr Lys Arg Gln Leu Leu Ala Glu Arg Gln Lys Arg Ile Glu  
 385 390 395 400

Gln Gln Lys Glu Gln Arg Arg Arg Leu Glu Glu Gln Gln Arg Arg Glu  
 405 410 415

Arg Glu Ala Arg Arg Gln Gln Glu Arg Glu Gln Arg Arg Arg Glu Gln  
 420 425 430

Glu Glu Lys Arg Arg Leu Glu Glu Leu Glu Arg Arg Arg Lys Glu Glu  
 435 440 445

Glu Glu Arg Arg Arg Ala Glu Glu Glu Lys Arg Arg Val Glu Arg Glu  
 450 455 460

Gln Glu Tyr Ile Arg Arg Gln Leu Glu Glu Glu Gln Arg His Leu Glu  
 465 470 475 480

Val Leu Gln Gln Gln Leu Leu Gln Glu Gln Ala Met Leu Leu His Asp  
 485 490 495

His Arg Arg Pro His Pro Gln His Ser Gln Gln Pro Pro Pro Pro Gln  
 500 505 510

Gln Glu Arg Ser Lys Pro Ser Phe His Ala Pro Glu Pro Lys Ala His  
 515 520 525

Tyr Glu Pro Ala Asp Arg Ala Arg Glu Val Pro Val Arg Thr Thr Ser  
 530 535 540

Arg Ser Pro Val Leu Ser Arg Arg Asp Ser Pro Leu Gln Gly Ser Gly  
 545 550 555 560

Gln Gln Asn Ser Gln Ala Gly Gln Arg Asn Ser Thr Ser Ser Ile Glu  
 565 570 575

Pro Arg Leu Leu Trp Glu Arg Val Glu Lys Leu Val Pro Arg Pro Gly  
 580 585 590

Ser Gly Ser Ser Ser Gly Ser Ser Asn Ser Gly Ser Gln Pro Gly Ser  
 595 600 605

His Pro Gly Ser Gln Ser Gly Ser Gly Glu Arg Phe Arg Val Arg Ser  
 610 615 620

Ser Ser Lys Ser Glu Gly Ser Pro Ser Gln Arg Leu Glu Asn Ala Val  
 625 630 635 640

Lys Lys Pro Glu Asp Lys Lys Glu Val Phe Arg Pro Leu Lys Pro Ala  
 645 650 655

Gly Glu Val Asp Leu Thr Ala Leu Ala Lys Glu Leu Arg Ala Val Glu  
 660 665 670

Asp Val Arg Pro Pro His Lys Val Thr Asp Tyr Ser Ser Ser Ser Glu  
 675 680 685

Glu Ser Gly Thr Thr Asp Glu Glu Asp Asp Asp Val Glu Gln Glu Gly  
 690 695 700

Ala Asp Glu Ser Thr Ser Gly Pro Glu Asp Thr Arg Ala Ala Ser Ser  
 705 710 715 720

Leu Asn Leu Ser Asn Gly Glu Thr Glu Ser Val Lys Thr Met Ile Val  
 725 730 735

His Asp Asp Val Glu Ser Glu Pro Ala Met Thr Pro Ser Lys Glu Gly  
 740 745 750

Thr Leu Ile Val Arg Gln Thr Gln Ser Ala Ser Ser Thr Leu Gln Lys  
 755 760 765

His Lys Ser Ser Ser Ser Phe Thr Pro Phe Ile Asp Pro Arg Leu Leu  
 770 775 780

Gln Ile Ser Pro Ser Ser Gly Thr Thr Val Thr Ser Val Val Gly Phe  
 785 790 795 800

Ser Cys Asp Gly Met Arg Pro Glu Ala Ile Arg Gln Asp Pro Thr Arg  
 805 810 815

Lys Gly Ser Val Val Asn Val Asn Pro Thr Asn Thr Arg Pro Gln Ser  
 820 825 830

Asp Thr Pro Glu Ile Arg Lys Tyr Lys Lys Arg Phe Asn Ser Glu Ile



835	840	845
Leu Cys Ala Ala Leu Trp Gly Val Asn Leu Leu Val Gly Thr Glu Ser		
850	855	860
Gly Leu Met Leu Leu Asp Arg Ser Gly Gln Gly Lys Val Tyr Pro Leu		
865	870	875 880
Ile Asn Arg Arg Arg Phe Gln Gln Met Asp Val Leu Glu Gly Leu Asn		
	885	890 895
Val Leu Val Thr Ile Ser Gly Lys Lys Asp Lys Leu Arg Val Tyr Tyr		
	900	905 910
Leu Ser Trp Leu Arg Asn Lys Ile Leu His Asn Asp Pro Glu Val Glu		
	915	920 925
Lys Lys Gln Gly Trp Thr Thr Val Gly Asp Leu Glu Gly Cys Val His		
	930	935 940
Tyr Lys Val Val Lys Tyr Glu Arg Ile Lys Phe Leu Val Ile Ala Leu		
	945	950 955 960
Lys Ser Ser Val Glu Val Tyr Ala Trp Ala Pro Lys Pro Tyr His Lys		
	965	970 975
Phe Met Ala Phe Lys Ser Phe Gly Glu Leu Val His Lys Pro Leu Leu		
	980	985 990
Val Asp Leu Thr Val Glu Glu Gly Gln Arg Leu Lys Val Ile Tyr Gly		
	995	1000 1005
Ser Cys Ala Gly Phe His Ala Val Asp Val Asp Ser Gly Ser Val		
	1010	1015 1020
Tyr Asp Ile Tyr Leu Pro Thr His Val Arg Lys Asn Pro His Ser		
	1025	1030 1035
Met Ile Gln Cys Ser Ile Lys Pro His Ala Ile Ile Ile Leu Pro		
	1040	1045 1050
Asn Thr Asp Gly Met Glu Leu Leu Val Cys Tyr Glu Asp Glu Gly		
	1055	1060 1065
Val Tyr Val Asn Thr Tyr Gly Arg Ile Thr Lys Asp Val Val Leu		
	1070	1075 1080

Gln Trp Gly Glu Met Pro Thr Ser Val Ala Tyr Ile Arg Ser Asn  
 1085 1090 1095

Gln Thr Met Gly Trp Gly Glu Lys Ala Ile Glu Ile Arg Ser Val  
 1100 1105 1110

Glu Thr Gly His Leu Asp Gly Val Phe Met His Lys Arg Ala Gln  
 1115 1120 1125

Arg Leu Lys Phe Leu Cys Glu Arg Asn Asp Lys Val Phe Phe Ala  
 1130 1135 1140

Ser Val Arg Ser Gly Gly Ser Ser Gln Val Tyr Phe Met Thr Leu  
 1145 1150 1155

Gly Arg Thr Ser Leu Leu Ser Trp  
 1160 1165

<210> 9  
 <211> 1239  
 <212> PRT  
 <213> HUMAN

<400> 9

Met Ala Asn Asp Ser Pro Ala Lys Ser Leu Val Asp Ile Asp Leu Ser  
 1 5 10 15

Ser Leu Arg Asp Pro Ala Gly Ile Phe Glu Leu Val Glu Val Val Gly  
 20 25 30

Asn Gly Thr Tyr Gly Gln Val Tyr Lys Gly Arg His Val Lys Thr Gly  
 35 40 45

Gln Leu Ala Ala Ile Lys Val Met Asp Val Thr Glu Asp Glu Glu Glu  
 50 55 60

Glu Ile Lys Leu Glu Ile Asn Met Leu Lys Lys Tyr Ser His His Arg  
 65 70 75 80

Asn Ile Ala Thr Tyr Tyr Gly Ala Phe Ile Lys Lys Ser Pro Pro Gly  
 85 90 95

His Asp Asp Gln Leu Trp Leu Val Met Glu Phe Cys Gly Ala Gly Ser  
 100 105 110

Ile Thr Asp Leu Val Lys Asn Thr Lys Gly Asn Thr Leu Lys Glu Asp  
 115 120 125

Trp Ile Ala Tyr Ile Ser Arg Glu Ile Leu Arg Gly Leu Ala His Leu  
 130 135 140

His Ile His His Val Ile His Arg Asp Ile Lys Gly Gln Asn Val Leu  
 145 150 155 160

Leu Thr Glu Asn Ala Glu Val Lys Leu Val Asp Phe Gly Val Ser Ala  
 165 170 175

Gln Leu Asp Arg Thr Val Gly Arg Arg Asn Thr Phe Ile Gly Thr Pro  
 180 185 190

Tyr Trp Met Ala Pro Glu Val Ile Ala Cys Asp Glu Asn Pro Asp Ala  
 195 200 205

Thr Tyr Asp Tyr Arg Ser Asp Leu Trp Ser Cys Gly Ile Thr Ala Ile  
 210 215 220

Glu Met Ala Glu Gly Ala Pro Pro Leu Cys Asp Met His Pro Met Arg  
 225 230 235 240

Ala Leu Phe Leu Ile Pro Arg Asn Pro Pro Pro Arg Leu Lys Ser Lys  
 245 250 255

Lys Trp Ser Lys Lys Phe Phe Ser Phe Ile Glu Gly Cys Leu Val Lys  
 260 265 270

Asn Tyr Met Gln Arg Pro Ser Thr Glu Gln Leu Leu Lys His Pro Phe  
 275 280 285

Ile Arg Asp Gln Pro Asn Glu Arg Gln Val Arg Ile Gln Leu Lys Asp  
 290 295 300

His Ile Asp Arg Thr Arg Lys Lys Arg Gly Glu Lys Asp Glu Thr Glu  
 305 310 315 320

Tyr Glu Tyr Ser Gly Ser Glu Glu Glu Glu Glu Glu Val Pro Glu Gln  
 325 330 335

Glu Gly Glu Pro Ser Ser Ile Val Asn Val Pro Gly Glu Ser Thr Leu  
 340 345 350

Arg Arg Asp Phe Leu Arg Leu Gln Gln Glu Asn Lys Glu Arg Ser Glu

355	360	365
Ala Leu Arg Arg Gln Gln Leu Leu Gln Glu Gln Gln Leu Arg Glu Gln		
370	375	380
Glu Glu Tyr Lys Arg Gln Leu Leu Ala Glu Arg Gln Lys Arg Ile Glu		
385	390	400
Gln Gln Lys Glu Gln Arg Arg Arg Leu Glu Glu Gln Gln Arg Arg Glu		
	405	410
Arg Glu Ala Arg Arg Gln Gln Glu Arg Glu Gln Arg Arg Arg Glu Gln		
	420	425
Glu Glu Lys Arg Arg Leu Glu Glu Leu Glu Arg Arg Arg Lys Glu Glu		
	435	440
Glu Glu Arg Arg Arg Ala Glu Glu Glu Lys Arg Arg Val Glu Arg Glu		
	450	455
Gln Glu Tyr Ile Arg Arg Gln Leu Glu Glu Glu Gln Arg His Leu Glu		
465	470	475
Val Leu Gln Gln Gln Leu Leu Gln Glu Gln Ala Met Leu Leu Glu Cys		
	485	490
Arg Trp Arg Glu Met Glu Glu His Arg Gln Ala Glu Arg Leu Gln Arg		
	500	505
Gln Leu Gln Gln Glu Gln Ala Tyr Leu Leu Ser Leu Gln His Asp His		
515	520	525
Arg Arg Pro His Pro Gln His Ser Gln Gln Pro Pro Pro Pro Gln Gln		
530	535	540
Glu Arg Ser Lys Pro Ser Phe His Ala Pro Glu Pro Lys Ala His Tyr		
545	550	555
Glu Pro Ala Asp Arg Ala Arg Glu Val Glu Asp Arg Phe Arg Lys Thr		
	565	570
Asn His Ser Ser Pro Glu Ala Gln Ser Lys Gln Thr Gly Arg Val Leu		
	580	585
Glu Pro Pro Val Pro Ser Arg Ser Glu Ser Phe Ser Asn Gly Asn Ser		
	595	600

Glu Ser Val His Pro Ala Leu Gln Arg Pro Ala Glu Pro Gln Val Pro  
610 615 620

Val Arg Thr Thr Ser Arg Ser Pro Val Leu Ser Arg Arg Asp Ser Pro  
625 630 635 640

Leu Gln Gly Ser Gly Gln Gln Asn Ser Gln Ala Gly Gln Arg Asn Ser  
645 650 655

Thr Ser Ile Glu Pro Arg Leu Leu Trp Glu Arg Val Glu Lys Leu Val  
660 665 670

Pro Arg Pro Gly Ser Gly Ser Ser Ser Gly Ser Ser Asn Ser Gly Ser  
675 680 685

Gln Pro Gly Ser His Pro Gly Ser Gln Ser Gly Ser Gly Glu Arg Phe  
690 695 700

Arg Val Arg Ser Ser Ser Lys Ser Glu Gly Ser Pro Ser Gln Arg Leu  
705 710 715 720

Glu Asn Ala Val Lys Lys Pro Glu Asp Lys Lys Glu Val Phe Arg Pro  
725 730 735

Leu Lys Pro Ala Asp Leu Thr Ala Leu Ala Lys Glu Leu Arg Ala Val  
740 745 750

Glu Asp Val Arg Pro Pro His Lys Val Thr Asp Tyr Ser Ser Ser Ser  
755 760 765

Glu Glu Ser Gly Thr Thr Asp Glu Glu Asp Asp Asp Val Glu Gln Glu  
770 775 780

Gly Ala Asp Glu Ser Thr Ser Gly Pro Glu Asp Thr Arg Ala Ala Ser  
785 790 795 800

Ser Leu Asn Leu Ser Asn Gly Glu Thr Glu Ser Val Lys Thr Met Ile  
805 810 815

Val His Asp Asp Val Glu Ser Glu Pro Ala Met Thr Pro Ser Lys Glu  
820 825 830

Gly Thr Leu Ile Val Arg Arg Thr Gln Ser Ala Ser Ser Thr Leu Gln  
835 840 845

Lys His Lys Ser Ser Ser Ser Phe Thr Pro Phe Ile Asp Pro Arg Leu  
850 855 860

Leu Gln Ile Ser Pro Ser Ser Gly Thr Thr Val Thr Ser Val Val Gly  
865 870 875 880

Phe Ser Cys Asp Gly Met Arg Pro Glu Ala Ile Arg Gln Asp Pro Thr  
885 890 895

Arg Lys Gly Ser Val Val Asn Val Asn Pro Thr Asn Thr Arg Pro Gln  
900 905 910

Ser Asp Thr Pro Glu Ile Arg Lys Tyr Lys Lys Arg Phe Asn Ser Glu  
915 920 925

Ile Leu Cys Ala Ala Leu Trp Gly Val Asn Leu Leu Val Gly Thr Glu  
930 935 940

Ser Gly Leu Met Leu Leu Asp Arg Ser Gly Gln Gly Lys Val Tyr Pro  
945 950 955 960

Leu Ile Asn Arg Arg Arg Phe Gln Gln Met Asp Val Leu Glu Gly Leu  
965 970 975

Asn Val Leu Val Thr Ile Ser Gly Lys Lys Asp Lys Leu Arg Val Tyr  
980 985 990

Tyr Leu Ser Trp Leu Arg Asn Lys Ile Leu His Asn Asp Pro Glu Val  
995 1000 1005

Glu Lys Lys Gln Gly Trp Thr Thr Val Gly Asp Leu Glu Gly Cys  
1010 1015 1020

Val His Tyr Lys Val Val Lys Tyr Glu Arg Ile Lys Phe Leu Val  
1025 1030 1035

Ile Ala Leu Lys Ser Ser Val Glu Val Tyr Ala Trp Ala Pro Lys  
1040 1045 1050

Pro Tyr His Lys Phe Met Ala Phe Lys Ser Phe Gly Glu Leu Val  
1055 1060 1065

His Lys Pro Leu Leu Val Asp Leu Thr Val Glu Glu Gly Gln Arg  
1070 1075 1080

Leu Lys Val Ile Tyr Gly Ser Cys Ala Gly Phe His Ala Val Asp  
 1085 1090 1095

Val Asp Ser Gly Ser Val Tyr Asp Ile Tyr Leu Pro Thr His Ile  
 1100 1105 1110

Gln Cys Ser Ile Lys Pro His Ala Ile Ile Ile Leu Pro Asn Thr  
 1115 1120 1125

Asp Gly Met Glu Leu Leu Val Cys Tyr Glu Asp Glu Gly Val Tyr  
 1130 1135 1140

Val Asn Thr Tyr Gly Arg Ile Thr Lys Asp Val Val Leu Gln Trp  
 1145 1150 1155

Gly Glu Met Pro Thr Ser Val Ala Tyr Ile Arg Ser Asn Gln Thr  
 1160 1165 1170

Met Gly Trp Gly Glu Lys Ala Ile Glu Ile Arg Ser Val Glu Thr  
 1175 1180 1185

Gly His Leu Asp Gly Val Phe Met His Lys Arg Ala Gln Arg Leu  
 1190 1195 1200

Lys Phe Leu Cys Glu Arg Asn Asp Lys Val Phe Phe Ala Ser Val  
 1205 1210 1215

Arg Ser Gly Gly Ser Ser Gln Val Tyr Phe Met Thr Leu Gly Arg  
 1220 1225 1230

Thr Ser Leu Leu Ser Trp  
 1235

<210> 10  
 <211> 504  
 <212> PRT  
 <213> HUMAN

<400> 10

Met Ala Ala Gln Arg Arg Ser Leu Leu Gln Ser Glu Gln Gln Pro Ser  
 1 5 10 15

Trp Thr Asp Asp Leu Pro Leu Cys His Leu Ser Gly Val Gly Ser Ala  
 20 25 30

Ser Asn Arg Ser Tyr Ser Ala Asp Gly Lys Gly Thr Glu Ser His Pro  
 35 40 45

Pro Glu Asp Ser Trp Leu Lys Phe Arg Ser Glu Asn Asn Cys Phe Leu  
 50 55 60

Tyr Gly Val Phe Asn Gly Tyr Asp Gly Asn Arg Val Thr Asn Phe Val  
 65 70 75 80

Ala Gln Arg Leu Ser Ala Glu Leu Leu Leu Gly Gln Leu Asn Ala Glu  
 85 90 95

His Ala Glu Ala Asp Val Arg Arg Val Leu Leu Gln Ala Phe Asp Val  
 100 105 110

Val Glu Arg Ser Phe Leu Glu Ser Ile Asp Asp Ala Leu Ala Glu Lys  
 115 120 125

Ala Ser Leu Gln Ser Gln Leu Pro Glu Gly Val Pro Gln His Gln Leu  
 130 135 140

Pro Pro Gln Tyr Gln Lys Ile Leu Glu Arg Leu Lys Thr Leu Glu Arg  
 145 150 155 160

Glu Ile Ser Gly Gly Ala Met Ala Val Val Ala Val Leu Leu Asn Asn  
 165 170 175

Lys Leu Tyr Val Ala Asn Val Gly Thr Asn Arg Ala Leu Leu Cys Lys  
 180 185 190

Ser Thr Val Asp Gly Leu Gln Val Thr Gln Leu Asn Val Asp His Thr  
 195 200 205

Thr Glu Asn Glu Asp Glu Leu Phe Arg Leu Ser Gln Leu Gly Leu Asp  
 210 215 220

Ala Gly Lys Ile Lys Gln Val Gly Ile Ile Cys Gly Gln Glu Ser Thr  
 225 230 235 240

Arg Arg Ile Gly Asp Tyr Lys Val Lys Tyr Gly Tyr Thr Asp Ile Asp  
 245 250 255

Leu Leu Ser Ala Ala Lys Ser Lys Pro Ile Ile Ala Glu Pro Glu Ile  
 260 265 270

His Gly Ala Gln Pro Leu Asp Gly Val Thr Gly Phe Leu Val Leu Met  
 275 280 285



Ser Glu Gly Leu Tyr Lys Ala Leu Glu Ala Ala His Gly Pro Gly Gln  
 290 295 300

Ala Asn Gln Glu Ile Ala Ala Met Ile Asp Thr Glu Phe Ala Lys Gln  
 305 310 315 320

Thr Ser Leu Asp Ala Val Ala Gln Ala Val Val Asp Arg Val Lys Arg  
 325 330 335

Ile His Ser Asp Thr Phe Ala Ser Gly Gly Glu Arg Ala Arg Phe Cys  
 340 345 350

Pro Arg His Glu Asp Met Thr Leu Leu Val Arg Asn Phe Gly Tyr Pro  
 355 360 365

Leu Gly Glu Met Ser Gln Pro Thr Pro Ser Pro Ala Pro Ala Ala Gly  
 370 375 380

Gly Arg Val Tyr Pro Val Ser Val Pro Tyr Ser Ser Ala Gln Ser Thr  
 385 390 395 400

Ser Lys Thr Ser Val Thr Leu Ser Leu Val Met Pro Ser Gln Gly Gln  
 405 410 415

Met Val Asn Gly Ala His Ser Ala Ser Thr Leu Asp Glu Ala Thr Pro  
 420 425 430

Thr Leu Thr Asn Gln Ser Pro Thr Leu Thr Leu Gln Ser Thr Asn Thr  
 435 440 445

His Thr Gln Ser Ser Ser Ser Ser Ser Asp Gly Gly Leu Phe Arg Ser  
 450 455 460

Arg Pro Ala His Ser Leu Pro Pro Gly Glu Asp Gly Arg Val Glu Pro  
 465 470 475 480

Tyr Val Asp Phe Ala Glu Phe Tyr Arg Leu Trp Ser Val Asp His Gly  
 485 490 495

Glu Gln Ser Val Val Thr Ala Pro  
 500

<210> 11  
 <211> 427  
 <212> PRT  
 <213> HUMAN

<400> 11

Met Ser Arg Ser Lys Arg Asp Asn Asn Phe Tyr Ser Val Glu Ile Gly  
1 5 10 15

Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr Gln Asn Leu Lys Pro Ile  
20 25 30

Gly Ser Gly Ala Gln Gly Ile Val Cys Ala Ala Tyr Asp Ala Ile Leu  
35 40 45

Glu Arg Asn Val Ala Ile Lys Lys Leu Ser Arg Pro Phe Gln Asn Gln  
50 55 60

Thr His Ala Lys Arg Ala Tyr Arg Glu Leu Val Leu Met Lys Cys Val  
65 70 75 80

Asn His Lys Asn Ile Ile Gly Leu Leu Asn Val Phe Thr Pro Gln Lys  
85 90 95

Ser Leu Glu Glu Phe Gln Asp Val Tyr Ile Val Met Glu Leu Met Asp  
100 105 110

Ala Asn Leu Cys Gln Val Ile Gln Met Glu Leu Asp His Glu Arg Met  
115 120 125

Ser Tyr Leu Leu Tyr Gln Met Leu Cys Gly Ile Lys His Leu His Ser  
130 135 140

Ala Gly Ile Ile His Arg Asp Leu Lys Pro Ser Asn Ile Val Val Lys  
145 150 155 160

Ser Asp Cys Thr Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg Thr Ala  
165 170 175

Gly Thr Ser Phe Met Met Thr Pro Tyr Val Val Thr Arg Tyr Tyr Arg  
180 185 190

Ala Pro Glu Val Ile Leu Gly Met Gly Tyr Lys Glu Asn Val Asp Leu  
195 200 205

Trp Ser Val Gly Cys Ile Met Gly Glu Met Val Cys His Lys Ile Leu  
210 215 220

Phe Pro Gly Arg Asp Tyr Ile Asp Gln Trp Asn Lys Val Ile Glu Gln  
225 230 235 240

Leu Gly Thr Pro Cys Pro Glu Phe Met Lys Lys Leu Gln Pro Thr Val  
 245 250 255

Arg Thr Tyr Val Glu Asn Arg Pro Lys Tyr Ala Gly Tyr Ser Phe Glu  
 260 265 270

Lys Leu Phe Pro Asp Val Leu Phe Pro Ala Asp Ser Glu His Asn Lys  
 275 280 285

Leu Lys Ala Ser Gln Ala Arg Asp Leu Leu Ser Lys Met Leu Val Ile  
 290 295 300

Asp Ala Ser Lys Arg Ile Ser Val Asp Glu Ala Leu Gln His Pro Tyr  
 305 310 315 320

Ile Asn Val Trp Tyr Asp Pro Ser Glu Ala Glu Ala Pro Pro Pro Lys  
 325 330 335

Ile Pro Asp Lys Gln Leu Asp Glu Arg Glu His Thr Ile Glu Glu Trp  
 340 345 350

Lys Glu Leu Ile Tyr Lys Glu Val Met Asp Leu Glu Glu Arg Thr Lys  
 355 360 365

Asn Gly Val Ile Arg Gly Gln Pro Ser Pro Leu Gly Ala Ala Val Ile  
 370 375 380

Asn Gly Ser Gln His Pro Ser Ser Ser Ser Val Asn Asp Val Ser  
 385 390 395 400

Ser Met Ser Thr Asp Pro Thr Leu Ala Ser Asp Thr Asp Ser Ser Leu  
 405 410 415

Glu Ala Ala Ala Gly Pro Leu Gly Cys Cys Arg  
 420 425

<210> 12  
 <211> 2909  
 <212> DNA  
 <213> Human

<400> 12  
 tggccgcggg agccgggacg gcgggccccg cttccggccc gggcgctcgtg cgtgaccacg 60  
 cggcgtcaca gccgaggaag cggccccggc gggagggcgg ggagggcgcg cggcgatcgg 120  
 acacgatggc gggaggaggc gggagtagcg acggcagcgg gcgggcagct ggcaggcggg 180

cgtcccgag tagcgggcg gcccggcg ggcgccag gccggggctg gggggcccg	240
cggagcgcg cgcgggggag gcacggctgg aagaggcagt caatcgctgg gtgctcaagt	300
tctacttcca cgaggcgctg cgggcctttc ggggtagccg gtacggggac ttcagacaga	360
tccgggacat catgcaggct ttgcttgtca ggcccttggg gaaggagcac accgtgtccc	420
gattgctgcg ggttatgcag tgtctgtcgc ggattgaaga aggggaaaat ttagactggt	480
cctttgatat ggaggctgag ctcacaccac tggaatcagc tatcaatgtg ctggagatga	540
ttaaaacgga atttacactg acagaagcag tggtcgaatc cagtagaaaa ctggtcaagg	600
aagctgctgt cattatattgt atcaaaaaca aagaatttga aaaggcttca aaaattttga	660
aaaaacatat gtccaaggac cccacaactc agaagctgag aaatgatctc ctgaatatta	720
ttcgagaaaa gaacttggcc catcctgtta tccagaactt ttcatatgag accttcagc	780
agaagatgct gcgcttcctg gagagccacc tggatgacgc cgagccctac ctctcacga	840
tggccaaaaa ggctttgaaa tctgagtccg ctgcctcaag tacagggaag gaagataaac	900
agccagcacc agggcctgtg gaaaagccac ccagagaacc cgcaaggcag ctacggaatc	960
ctccaaccac cattggaatg atgactctga aagcagcttt caagactctg tctggtgcac	1020
aggattctga ggcagccttt gcaaaactgg accagaagga tctggttctt cctactcaag	1080
ctctcccagc atcaccagcc ctcaaaaaca agagaccagc aaaagatgaa aacgaaagtt	1140
cagccccggc tgacggtgag ggtggctcgg aactgcagcc caagaacaag cgcagtacaa	1200
taagcagatt ggtcttgag gaggacagcc agagtactga gccagcgca ggcctcaact	1260
cctcccagga ggccgcttca gcgccaccat ccaagccac cgcttctaac caaccctcc	1320
ctggagagaa gaatcccaa gtacccaaag gcaagtggaa cagctctaag ggggttgaag	1380
aaaaggagac ttgggtggaa gaggatgaac tgtttcaagt tcaggcagca ccagatgaag	1440
acagtacaac caatataaca aaaaagcaga agtggactgt agaagaaagc gagtgggtca	1500
aggctggagt gcagaaatat ggggaaggaa actgggctgc catttctaaa aattacccat	1560
ttgttaaccg aacagctgtg atgattaagg atcgctggcg gaccatgaaa agacttggca	1620
tgaactgaaa caggctttca tttccacaga attcacagga gcatgggtcc taataatagc	1680
ccctgatagt ctgctctttc tttctttttc tttttttttt ttttttgaga cagagtctcg	1740
ctctgtcacc caggctggag tgcagtggcg tgatctcggc tcaactgcgac ctccgtctcc	1800
cgggctcacg ccattctcct gcctcagcct cccgagtagc tgggactaca ggcgcccgc	1860
atcacgccc gctaattgtt tgtattttta gtagagacgg ggtttcacccg tgttagccag	1920
gatggtctcg atctcctgac ctgctgatcc acccaactcg gcctcccaa gtgctgggat	1980

tacaggcatg agccaccgcg cctggcatct gctgtttctt tcagaagctg ggctgggatg	2040
agaatTTTTg gcaacctcct tcgacgtggg ggaggtccca tttccacttc atcactgttg	2100
gagatcatgg agctaagaag cagagccaag tccacccatg tccttggcag agatgacagg	2160
cacacagctt gtgcagtgcc agaatatcat tagcgtttcc cttctttagt ggtttgctta	2220
aattttaaate cctggtaate tgtagaacct tctcctagga aatggggaag tctattagga	2280
gccacttggtg actccatgac ctgttaaaac cagcaatgtg agtattattt ggagtaaatt	2340
tggtccacgt caagttctgg ccttctgatg caaatgcaaa ggaacttagt ctgttatgaa	2400
cccagggtga tgacagacca gtccttgtgg aataagattc cctttaaaaa ctctttagcc	2460
agtcgtgaca tcaaccctag acctgtctgc cttggcattt gctgtcaaca tctgctgggc	2520
tatgtaggca ggtaatcct ccactttctca tgtggttgaa ccagtgtgtt ttttggtaaa	2580
atgggtgattg tagataagat tagttccctg atcccctgcc ccctgtcccc tgccctctttt	2640
cccaattccc ttccttatgc tggactttta aagcttaaaa aaaatccgat tgaatataaa	2700
tgccataattt cattctttgt gaaatgggtg cttcctcctg attccctaata tgtgctgtgt	2760
tcgtgtcttg cactggaatt caacattccc ttctcctttt gtactgtgtt gtgcttgctg	2820
tctctcccgg acacccttaa agactgtctt tttagcaaaa aatttcagta aagtgttttc	2880
tgtaatcttt ttttaaaaaa aaaaaaaaaa	2909

<210> 13  
 <211> 2547  
 <212> DNA  
 <213> Human

<400> 13	
cttacaagggt acagtcctct gctcaggggg gccaggaggg tcttataggc atcattcacc	60
agggtcgaat gcttctctga gaagtccttt tcagttctgag acctctggct gaagaaatct	120
gggtggacaa gacgctgcag ttgctggtac ctgtgctgga gcttcgctgt atcaactctg	180
aaggaacgggt tgcagtccat aaggctgaag tagtctcgag tggggtcagg tgccctgcagc	240
gctcggcact gtgggcagaa gaacctgtcc tcccgcccgg ggcccatgg gccgccgcag	300
ttccaacagc ggggataatt gcttcccggc tgcgacgcag catcgagct tagcggctctc	360
cttctgggaa cccctgtcgg ccaaaacccc cacacccgga gcaaagcccc ggctctcccc	420
cgccacatct ggccggcggc ctatctagcc gtgggtcactc gtggggaaaa gcaaagagag	480
cgtctaacca gactaatgtt gctgattggc tggggagtcg agggggcggg atcacccgag	540
gggaacccgg gttctaagtt ccgctctccc ttctaaacta caactcccag gaggcattga	600
ggcggcgccct gacggccaca tctgctgctc ctcattgggc cggcggcagg ggaggggggtt	660

ttgattggct	gagggaggag	tttgtatctg	caggttttagc	gccactctgc	tggtgagggc	720
tgcgagagat	gtgcggctcc	aggtgggctc	acgcggctcg	gatgtctcgg	gagtcgggatg	780
ttgagggtca	gcagtctcat	ggcagcagtg	cctgttcaca	gccccatggc	agcgttaccc	840
agtcccaagg	ctcctctca	cagtcaccag	gcataatccag	ctcctctacc	agcacgatgc	900
caaactccag	ccagtcctct	cactccagct	ctgggacact	gagctcctta	gagacagtgt	960
ccactcagga	actctattct	attcctgagg	accaagaacc	tgaggaccaa	gaacctgagg	1020
agcctacccc	tgccccctgg	gctcgattat	gggcccttca	ggatggattt	gccaatcttg	1080
aatgtgtgaa	tgacaactac	tggtttggga	gggacaaaag	ctgtgaatat	tgctttgatg	1140
aacctgtgct	gaaaagaaca	gataaatacc	gaacatacag	caagaaacac	tttcggattt	1200
tcagggaagt	gggtcctaaa	aactcttaca	ttgcatacat	agaagatcac	agtggcaatg	1260
gaacctttgt	aaatacagag	cttgtaggga	aaggaaaacg	ccgtcctttg	aataacaatt	1320
ctgaaattgc	actgtcacta	agcagaaata	aagtttttgt	cttttttgat	ctgactgtag	1380
atgatcagtc	agtttatcct	aaggcattaa	gagatgaata	catcatgtca	aaaactcttg	1440
gaagtgggtgc	ctgtggagag	gtaaagctgg	ctttcgagag	gaaaacatgt	aagaaagtag	1500
ccataaagat	catcagcaaa	aggaagtttg	ctattgggtc	agcaagagag	gcagaccag	1560
ctctcaatgt	tgaaacagaa	atagaaattt	tgaaaaagct	aatcatcct	tgcatcatca	1620
agattaaaaa	cttttttgat	gcagaagatt	attatatgtg	tttggaattg	atggaagggg	1680
gagagctgtt	tgacaaagt	gtggggaata	aacgcctgaa	agaagctacc	tgcaagctct	1740
atttttacca	gatgtctctg	gctgtgcagt	accttcatga	aaacgggtatt	atacaccgtg	1800
acttaaagcc	agagaatgtt	ttactgtcat	ctcaagaaga	ggactgtctt	ataaagatta	1860
ctgatttttg	gcactccaag	attttgggag	agacctctct	catgagaacc	ttatgtggaa	1920
ccccaccta	cttggcgct	gaagttcttg	tttctgttg	gactgctggg	tataaccgtg	1980
ctgtggactg	ctggagttta	ggagttatct	tttttatctg	ccttagtggg	tatccacctt	2040
tctctgagca	taggactcaa	gtgtcactga	aggatcagat	caccagtggg	aaatacaact	2100
tcattcctga	agtctgggca	gaagtctcag	agaaagctct	ggaccttgct	aagaagtgtg	2160
tggtagtggg	tccaaaggca	cgttttacga	cagaagaagc	cttaagacac	ccgtggcttc	2220
aggatgaaga	catgaagaga	aagtttcaag	atcttctgtc	tgaggaaaat	gaatccacag	2280
ctctacccca	ggttctagcc	cagccttcta	ctagtcgaaa	gcggccccgt	gaaggggaag	2340
ccgaggggtgc	cgagaccaca	aagcgcccag	ctgtgtgtgc	tgctgtgttg	tgaactccgt	2400
ggtttgaaca	cgaaagaaat	gtaccttctt	tcactctgtc	atctttcttt	tctttgagtc	2460
tgttttttta	tagtttgtat	tttaattatg	ggaataattg	ctttttcaca	gtcactgatg	2520

tacaattaaa aacctgatgg aacctgg

2547

<210> 14

<211> 2460

<212> DNA

<213> Human

<400> 14

cttacaaggt acagtcctct gctcaggggg gccaggaggg tcttataggc atcattcacc	60
agggtcgaat gcttctctga gaagtccttt tcagtctgag acctctggct gaagaaatct	120
gggtggacaa gacgctgcag ttgctggtac ctgtgctgga gcttcgctgt atcaactctg	180
aaggaacggg tgcagtcctat aaggctgaag tagtctcgag tggggtcagg tgccctgcagc	240
gctcggcact gtgggcagaa gaacctgtcc tcccgcccgg gggcccatgg gccgcgcgag	300
ttccaacagc ggggataatt gcttcccggc tgcgacgcag catcgcagct tagcggctctc	360
cttctgggaa cccctgtcgg ccaaaacccc cacacccgga gcaaagcccc ggctctcccc	420
cgccacatct ggccggcggc ctatctagcc gtgggtcactc gtggggaaaa gcaaagagag	480
cgtctaacca gactaatgtt gctgattggc tggggagtcg agggggcggg atcacccgag	540
gggaaccggt gttctaagtt ccgctctccc ttctaaacta caactcccag gaggcattga	600
ggcggcgcct gacggccaca tctgctgctc ctcatgtgtc cggcggcagg ggaggggggtt	660
ttgattgggt gaggggtggag tttgtatctg caggtttagc gccactctgc tggctgaggc	720
tgcggagagt gtgcggctcc aggtgggctc acgcggctcg gatgtctcgg gagtcggatg	780
ttgagggtca gcagtctcat ggcagcagtg cctgttcaca gggccatggc agcgttaccc	840
agtcccaagg ctctctctca cagtcccagg gcataatccag ctctcttacc agcacgatgc	900
caaactccag ccagtcctct cactccagct ctgggacact gagctcctta gagacagtgt	960
ccactcagga actctattct attcctgagg accaagaacc tgaggaccaa gaacctgagg	1020
agcctacccc tgccccctgg gctcgattat gggcccttca ggatggattt gccaatcttg	1080
aatgtgtgaa tgacaactac tggtttgagg gggacaaaag ctgtgaatat tgctttgatg	1140
aacctgtgct gaaaagaaca gataaatacc gaacatacag caagaaacac tttcggattt	1200
tcagggaagt gggtcctaaa aactcttaca ttgcatacat agaagatcac agtggcaatg	1260
gaacctttgt aaatacagag cttgtaggga aaggaaaacg ccgtcctttg aataacaatt	1320
ctgaaattgc actgtcacta agcagaaata aagtttttgt cttttttgat ctgactgtag	1380
atgatcagtc agtttatcct aaggcattaa gagatgaata catcatgtca aaaactcttg	1440
gaagtgggtg ctgtggagag gtaaagctgg ctttcgagag gaaaacatgt aagaaagtag	1500
ccataaagat catcagcaaa aggaagtttg ctattgggtc agcaagagag gcagaccag	1560

ctctcaatgt	tgaaacagaa	atagaaat	tttgaaaaagct	aatcatcct	tgcatcatca	1620
agattaaaaa	cttttttgat	gcagaagatt	attatatattgt	tttggaattg	atggaagggg	1680
gagagctgtt	tgacaaagt	gtggggaata	aacgcctgaa	agaagctacc	tgcaagctct	1740
atttttacca	gatgctcttg	gctgtgcaga	ttactgattt	tgggcactcc	aagatttttg	1800
gagagacctc	tctcatgaga	accttatgtg	gaacccccac	ctacttggcg	cctgaagttc	1860
ttgtttctgt	tgggactgct	gggtataacc	gtgctgtgga	ctgctggagt	ttaggagtta	1920
ttctttttat	ctgccttagt	gggtatccac	ctttctctga	gcataggact	caagtgtcac	1980
tgaaggatca	gatcaccagt	ggaaaataca	acttcattcc	tgaagtctgg	gcagaagtct	2040
cagagaaagc	tctggacctt	gtcaagaagt	tgttggtagt	ggatccaaag	gcacgtttta	2100
cgacagaaga	agccttaaga	caccctgtgg	ttcaggatga	agacatgaag	agaaagtttc	2160
aagatcttct	gtctgaggaa	aatgaatcca	cagctctacc	ccaggttcta	gccagacctt	2220
ctactagtcg	aaagcggccc	cgtgaagggg	aagccgaggg	tgccgagacc	acaaagcgcc	2280
cagctgtgtg	tgctgctgtg	ttgtgaactc	cgtggtttga	acacgaaaga	aatgtacctt	2340
ctttcactct	gtcatctttc	ttttctttga	gtctgttttt	ttatagtttg	tattttaatt	2400
atgggaataa	ttgctttttc	acagtcactg	atgtacaatt	aaaaacctga	tggaacctgg	2460

<210> 15  
 <211> 7171  
 <212> DNA  
 <213> HUMAN

<400> 15	
cacagagcga	cagagacatt
tattgttatt	tgttttttgg
tggcaaaaag	ggaaaatggc
60	
gaacgactcc	cctgcaaaaa
gtctgggtgga	catcgacctc
tcctccctgc	gggatcctgc
120	
tgggattttt	gagctggtgg
aagtgggttg	aaatggcacc
tatggacaag	tctataaggg
180	
tcgacatggt	aaaacgggtc
agttggcagc	catcaaagtt
atggatgtca	ctgaggatga
240	
agaggaagaa	atcaaactgg
agataaatat	gctaaagaaa
tactctcatc	acagaaacat
300	
tgcaacatat	tatggtgctt
tcatcaaaaa	gagccctcca
ggacatgatg	accaactctg
360	
gcttgttatg	gagttctgtg
gggctgggtc	cattacagac
cttggtgaaga	acaccaaagg
420	
gaacacactc	aaagaagact
ggatcgctta	catctccaga
gaaatcctga	ggggactggc
480	
acatcttcac	attcatcatg
tgattcaccg	ggatatcaag
ggccagaatg	tgttgctgac
540	
tgagaatgca	gaggtgaaac
ttgttgactt	tgggtgtgagt
gctcagctgg	acaggactgt
600	
ggggcggaga	aatacgttca
taggcactcc	ctactggatg
gctcctgagg	tcatcgcttg
660	
tgatgagaac	ccagatgccca
cctatgatta	cagaagtgat
ctttggtctt	gtggcattac
720	



agccattgag atggcagaag gtgctcccc tctctgtgac atgcatccaa tgagagcact	780
gtttctcatt cccagaaacc ctctccccg gctgaagtca aaaaaatggt cgaagaagtt	840
ttttagtttt atagaaggggt gcctggtgaa gaattacatg cagcggccct ctacagagca	900
gcttttgaaa catcctttta taagggatca gccaaatgaa aggcaagtta gaatccagct	960
taaggatcat atagatcgta ccaggaagaa gagaggcgag aaagatgaaa ctgagtatga	1020
gtacagtggg agtgaggaag aagaggagga agtgcctgaa caggaaggag agccaagttc	1080
cattgtgaac gtgcctgggtg agtctactct tcgccgagat ttcttgagac tgcagcagga	1140
gaacaaggaa cgttccgagg ctcttcggag acaacagtta ctacaggagc aacagctccg	1200
ggagcaggaa gaatataaaa ggcaactgct ggcagagaga cagaagcgga ttgagcagca	1260
gaaagaacag aggcgacggc tagaagagca acaaaggaga gagcgggaag ctagaaggca	1320
gcaggaacgt gaacagcgaa ggagagaaca agaagaaaag aggcgtctag aggagttgga	1380
gagaaggcgc aaagaagaag aggagaggag acgggcagaa gaagaaaaga ggagagttga	1440
aagagaacag gagtatatca ggcgacagct agaagaggag cagcggcact tggaagtcct	1500
tcagcagcag ctgctccagg agcaggccat gttactgcat gaccatagga ggccgcaccc	1560
gcagcactcg cagcagccgc caccaccgca gcaggaaagg agcaagccaa gcttccatgc	1620
tcctgagccc aaagcccact acgagcctgc tgaccgagcg cgagaggtgg aagatagatt	1680
taggaaaact aaccacagct cccctgaagc ccagtctaag cagacaggca gagtattgga	1740
gccaccagtg ccttcccgat cagagtcttt ttccaatggc aactccgagt ctgtgcatcc	1800
cgccctgcag agaccagcgg agccacaggt tcctgtgaga acaacatctc gctcccctgt	1860
tctgtcccggt cgagattccc cactgcaggg cagtgggcag cagaatagcc aggaggaca	1920
gagaaactcc accagcagta ttgagcccag gcttctgtgg gagagagtgg agaagctgggt	1980
gccagacct ggcagtggca gtcctcagg gtccagcaac tcaggatccc agcccgggtc	2040
tcacctggg tctcagagtg gtcctgggga acgcttcaga gtgagatcat catccaagtc	2100
tgaaggctct ccatctcagc gcctggaaaa tgcagtgaaa aaacctgaag ataaaaagga	2160
agttttcaga cccctcaagc ctgctggcga agtggatctg accgcactgg ccaaagagct	2220
tcgagcagtg gaagatgtac ggccacctca caaagtaacg gactactcct catccagtga	2280
ggagtcgggg acgacggatg aggaggacga cgatgtggag caggaagggg ctgacgagtc	2340
cacctcagga ccagaggaca ccagagcagc gtcactctctg aatttgagca atggtgaaac	2400
ggaatctgtg aaaaccatga ttgtccatga tgatgtagaa agtgagccgg ccatgacccc	2460
atccaaggag ggcactctaa tcgtccgcca gactcagtc gctagtagca cactccagaa	2520

acacaaatct	tcctcctcct	ttacaccttt	tatagacccc	agattactac	agattttctcc	2580
atctagcggg	acaacagtga	catctgtggt	gggattttcc	tgtgatggga	tgagaccaga	2640
agccataagg	caagatccta	cccggaaagg	ctcagtggtc	aatgtgaatc	ctaccaaacac	2700
taggccacag	agtgacaccc	cggagattcg	taaatacaag	aagaggttta	actctgagat	2760
tctgtgtgct	gccttatggg	gagtgaattt	gctagtgggt	acagagagtg	gcctgatgct	2820
gctggacaga	agtggccaag	ggaaggtcta	tcctcttata	aaccgaagac	gatttcaaca	2880
aatggacgta	cttgagggct	tgaatgtctt	ggtgacaata	tctggcaaaa	aggataagtt	2940
acgtgtctac	tatttgtcct	ggttaagaaa	taaaatactt	cacaatgata	cagaagttga	3000
gaagaagcag	ggatggacaa	ccgtagggga	tttggaagga	tgtgtacatt	ataaagttgt	3060
aaaatatgaa	agaatcaaat	ttctggtgat	tgctttgaag	agttctgtgg	aagtctatgc	3120
gtgggcacca	aagccatata	acaaatttat	ggcctttaag	tcatttggag	aattggtaca	3180
taagccatta	ctggtggata	tcactgttga	ggaaggccag	aggttgaaag	tgatctatgg	3240
atcctgtgct	ggattccatg	ctgttgatgt	ggattcagga	tcagtctatg	acatttatct	3300
accaacacat	atccagtgtg	gcatcaaacc	ccatgcaatc	atcatcctcc	ccaatacaga	3360
tggaatggag	cttctggtgt	gctatgaaga	tgaggggggt	tatgtaaaca	catatggaag	3420
gatcaccaag	gatgtagttc	tacagtgggg	agagatgcct	acatcagtag	catatatctg	3480
atccaatcag	acaatgggct	ggggagagaa	ggccatagag	atccgatctg	tggaactggg	3540
tcacttggat	ggtgtgttca	tgcacaaaag	ggctcaaaga	ctaaaattct	tgtgtgaacg	3600
caatgacaag	gtgttctttg	cctctgttcg	gtctggtggc	agcagtcagg	tttatttcat	3660
gaccttaggc	aggacttctc	ttctgagctg	gtagaagcag	tgtgatccag	ggattactgg	3720
cctccagagt	cttcaagata	ctgagaactt	ggaattcctt	gtaactggag	ctcggagctg	3780
caccgagggc	aaccaggaca	gctgtgtgtg	cagacctcat	gtgttggggt	ctctcccctc	3840
cttctgttgc	ctcttatata	ccagtttata	cccattcttt	ttttttttct	tactccaaaa	3900
taaatcaagg	ctgcaatgca	gctggtgctg	ttcagattct	accatcaggt	gctataagtg	3960
tttgggattg	agcatcatac	tggaagcaa	acacctttcc	tccagctcca	gaattccttg	4020
tctctgaatg	actctgtctt	gtgggtgtct	gacagtggcg	acgatgaaca	tgccgttggg	4080
tttattggca	gtgggcacaa	ggaggtgaga	agtggtggtg	aaaggagcgg	agtgtgaag	4140
cagagagcag	atttaatatg	gtaacattaa	cagtgtattt	aattgacatt	tcttttttgt	4200
aatgtgacga	tatgtggaca	aagaagaaga	tgacaggttt	agaagttaat	atttataaaa	4260
tgtgaaagac	acagttacta	ggataaactt	tttgtgggtg	gggcttggga	gatgggggtg	4320
ggtgggttaa	ggggtcccat	tttgtttctt	tggatttggg	gtgggggtcc	tgccaagaa	4380

ctcagtcatt	tttctgtgta	ccaggttgcc	taaatcatgt	gcagatgggt	ctaaaaaaaa	4440
aaaaaaaaaa	aaaaaaaaaa	ggaaaaaaaa	aaagaaaaag	aaaacgtgtg	catttttgtat	4500
aatggccaga	actttgtcgt	gtgacagtat	tagcactgcc	tcagttaaag	gttttaatttt	4560
tgtttaaacc	tagacgtgca	acaaaagttt	taccacagtc	tgacttgca	gaagaaagaa	4620
aaaaattcaa	accacatggt	tatTTTTTTTT	ttgcctacct	cattgttctt	aatgcattga	4680
gaggtgattt	agtttatatg	tttttggaag	aaaccattaa	tgtttaattt	aatcttaata	4740
ccaaaacgac	cagattgaag	tttgactttt	attgtcacaa	atcagcaggc	acaagaactg	4800
tccatgaaga	tgggaaatag	ccttaaggct	gatgcagttt	acttacaagt	ttagaaacca	4860
gaatgctttg	tttttaccag	attcaccatt	agaggttgat	ggggcaactg	cagcccatga	4920
cacaagatct	cattgttctc	gatgtagagg	ggttggtagc	agacagggtg	ttacattaga	4980
atagtcacac	aaactgttca	gtggtgcagg	aaccttttct	tgggggtggg	ggagtttccc	5040
ttttctaaaa	atgcaatgca	ctaaaactat	tttaagaatg	tagttaattc	tgcttattca	5100
taaagtgggc	atcttctgtg	ttttaggtgt	aatatcgaag	tcctggcttt	tctcgttttc	5160
tcacttgctc	tcttgttctc	tgTTTTTTTta	aaccaatttt	actttatgaa	tatattcatg	5220
acatttgtaa	taaatgtctt	gagaaagaat	ttgtttcatg	gcttcatggg	catcactcaa	5280
gtccccgtaa	ggatattacc	gtctcaggaa	aggatcagga	ctccatgtca	cagtcctgcc	5340
atcttacttt	cctcttgctg	agttctgagt	ggaaataact	gcattatggc	tgctttaacc	5400
tcagtcatca	aaagaaactt	gctgtttttt	aggcttgatc	tttttccttt	gtggttaatt	5460
ttcctgtata	ttgtgaaaat	gggggatttt	ccctctgctc	ccaccacact	aaacacagca	5520
gccatttgta	cctgtttgct	tcccatccca	cttggcacc	actctgacct	cttgtcagtt	5580
tctgttcct	ggttccatct	ttttgaaaaa	ggccctcctt	tgagctacaa	acatctggta	5640
agacaagtac	atccactcat	gaatgcagac	acagcagctg	gtggttttgt	gtatacctgt	5700
aaagacaagc	tgagaagctt	actttttggg	gaagtaaaag	aagatggaaa	tggatgtttc	5760
atttgatatga	gtttggagca	gtgctgaagg	ccaaagccgc	ctactggttt	gtagttaacc	5820
tagagaaggt	tgaaaaatta	atcctacctt	taaagggatt	tgaggtaggc	tggattccat	5880
cgccacagga	ctttagttag	aattaaattc	ctgcttgtaa	tttatatcca	tgtttaggct	5940
tttcataaga	tgaacatgc	cacagtgaac	acactcggtg	acatatcaag	agaagaagga	6000
aaggcacagg	tggagaacag	taaaaggtgg	gcagatgtct	ttgaagaaat	gctcaatgtc	6060
tgatgctaag	tgggagaagg	cagagaacaa	aggatgtggc	ataatggtct	taacattatc	6120
caaagacttg	aagctccatg	tctgtaagtc	aaatgttaca	caaaaaaaaa	tgcaaatggg	6180

gtttcattgg aattaccaag tgcttagaac ttgctggctt tcccataggt ggtaaagggg	6240
tctgagctca caccgagttg tgcttggctt gcttgtgcag ctccaggcac ccggtgggca	6300
ctctggtggt gtttgtggtg aactgaattg aatccattgt tgggcttaag ttactgaaat	6360
tggaacaccc tttgtccttc tggcgggggg ctctctggtc tgtgctttac ttggcttttt	6420
tccttcccgt cttagcctca ccccttgctc aaccagattg agttgctata gcttgatgca	6480
gggacccagt gaagtttctc cgtaaagat tgggagtcgt cgaaatgttt agattctttt	6540
aggaaaggaa ttattttccc cccttttaca gggtagtaac ttctccacag aagtgccaat	6600
atggcaaaat tacacaagaa aacagtattg caatgacacc attacataag gaacattgaa	6660
ctgttagagg agtgctcttc caaacaaaac aaaaatgtct ctaggtttag tcagagcttt	6720
cacaagtaat aacctttctg tattaataatc agagtaaccc tttctgtatt gagtgcagtg	6780
ttttttactc ttttctcatg cacatgttac gttggagaaa atgtttacaa aaatggtttt	6840
gttacactaa tgcgccaccac atatttatgg tttattttta gtgacttttt atgggttatt	6900
taggttttcg tcttagttgt agcacactta ccctaatttt gccattatt aatttgctaa	6960
atagtaatac aaatgacaaa ctgcattaaa tttactaatt ataaaagctg caaagcagac	7020
tggtggcaag tacacagccc ttttttttgc agtgctaact tgtctactgt gtattatgaa	7080
aattactgtt gtccccccac ccttttttcc ttaaataaag taaaaatgac acctaaaaaa	7140
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a	7171

<210> 16  
 <211> 7495  
 <212> DNA  
 <213> Human

<400> 16	
cacagagcga cagagacatt tattgttatt tgtttttttg tggcaaaaag ggaaaatggc	60
gaacgactcc cctgcaaaaa gtctggtgga catcgacctc tcctccctgc gggatcctgc	120
tgggattttt gagctggtgg aagtggttgg aaatggcacc tatggacaag tctataaggg	180
tcgacatggt aaaacgggtc agttggcagc catcaaagtt atggatgtca ctgaggatga	240
agaggaagaa atcaaactgg agataaatat gctaaagaaa tactctcatc acagaaacat	300
tgcaacatat tatggtgctt tcatcaaaaa gagccctcca ggacatgatg accaactctg	360
gcttgttatg gagttctgtg gggctgggtc cattacagac cttgtgaaga acaccaaagg	420
gaacacactc aaagaagact ggatcgctta catctccaga gaaatcctga ggggactggc	480
acatcttcac attcatcatg tgattcaccg ggatatcaag ggccagaatg tgttgctgac	540
tgagaatgca gaggtgaaac ttgttgactt tgggtgtgagt gctcagctgg acaggactgt	600

ggggcggaga	aatacgttca	taggcactcc	ctactggatg	gctcctgagg	tcacgcctg	660
tgatgagaac	ccagatgcca	cctatgatta	cagaagtgat	ctttggtctt	gtggcattac	720
agccattgag	atggcagaag	gtgctcccc	tctctgtgac	atgcatccaa	tgagagcact	780
gtttctcatt	cccagaaacc	ctcctccccg	gctgaagtca	aaaaaatggt	cgaagaagtt	840
ttttagtttt	atagaagggg	gcctggtgaa	gaattacatg	cagcggccct	ctacagagca	900
gcttttgaaa	catcctttta	taagggatca	gccaaatgaa	aggcaagtta	gaatccagct	960
taaggatcat	atagatcgta	ccaggaagaa	gagaggcgag	aaagatgaaa	ctgagtatga	1020
gtacagtggg	agtgaggaag	aagaggagga	agtgcctgaa	caggaaggag	agccaagttc	1080
cattgtgaac	gtgcctgggt	agtctactct	tcgccgagat	ttcctgagac	tgcagcagga	1140
gaacaaggaa	cgttccgagg	ctcttcggag	acaacagtta	ctacaggagc	aacagctccg	1200
ggagcaggaa	gaatataaaa	ggcaactgct	ggcagagaga	cagaagcgga	ttgagcagca	1260
gaaagaacag	aggcgacggc	tagaagagca	acaaaggaga	gagcgggaag	ctagaaggca	1320
gcaggaacgt	gaacagcgaa	ggagagaaca	agaagaaaag	aggcgtctag	aggagttaga	1380
gagaaggcgc	aaagaagaag	aggagaggag	acgggcagaa	gaagaaaaga	ggagagttga	1440
aagagaacag	gagtatatca	ggcgacagct	agaagaggag	cagcggcact	tggaaagtcct	1500
tcagcagcag	ctgctccagg	agcaggccat	gttactggag	tgccgatggc	gggagatgga	1560
ggagcaccgg	caggcagaga	ggctccagag	gcagttgcaa	caagaacaag	catatctcct	1620
gtctctacag	catgaccata	ggaggccgca	ccgcgagcac	tcgcagcagc	cgccaccacc	1680
gcagcaggaa	aggagcaagc	caagcttcca	tgctcccagag	cccaaagccc	actacgagcc	1740
tgctgaccga	gcgcgagagg	tggaagatag	atttaggaaa	actaaccaca	gctcccctga	1800
agcccagtct	aagcagacag	gcagagtatt	ggagccacca	gtgccttccc	gatcagagtc	1860
tttttccaat	ggcaactccg	agtctgtgca	tcccgccctg	cagagaccag	cggagccaca	1920
ggtacagtgg	tcccacctgg	catctctcaa	gaacaatggt	tcccctgtct	cgcgatccca	1980
ttccttcagt	gacccttctc	ccaaatttgc	acaccaccat	cttcgttctc	aggacccatg	2040
tccaccttcc	cgcagtgagg	tgctcagtca	gagctctgac	tctaagtcag	aggcgcctga	2100
ccctacccaa	aaggcttggt	ctagatcaga	cagtgaacgag	gtgcctccaa	gggttctctgt	2160
gagaacaaca	tctcgctccc	ctgttctgtc	ccgtcgagat	tccccactgc	agggcagtgg	2220
gcagcagaat	agccaggcag	gacagagaaa	ctccaccagc	agtattgagc	ccaggcttct	2280
gtgggagaga	gtggagaagc	tggtgcccag	acctggcagt	ggcagctcct	cagggtccag	2340
caactcagga	tcccagcccc	ggtctcacce	tgggtctcag	agtggctccg	gggaacgctt	2400
cagagtgaga	tcatcatcca	agtctgaagg	ctctccatct	cagcgcctgg	aaaatgcagt	2460

gaaaaaacct	gaagataaaa	aggaagtttt	cagaccctc	aagcctgctg	gcgaagtgga	2520
tctgaccgca	ctggccaaag	agcttcgagc	agtggaagat	gtacggccac	ctcaciaaagt	2580
aacggactac	tcctcatcca	gtgaggagtc	ggggacgacg	gatgaggagg	acgacgatgt	2640
ggagcaggaa	ggggctgacg	agtcacacctc	aggaccagag	gacaccagag	cagcgtcatc	2700
tctgaatttg	agcaatgggtg	aaacgggaatc	tgtgaaaacc	atgattgtcc	atgatgatgt	2760
agaaagtgag	ccggccatga	ccccatccaa	ggagggcact	ctaactgtcc	gccagactca	2820
gtccgctagt	agcacactcc	agaaacacaa	atcttctctc	tcctttacac	cttttataga	2880
cccagatta	ctacagattt	ctccatctag	cggacaaca	gtgacatctg	tggtgggatt	2940
ttcctgtgat	gggatgagac	cagaagccat	aaggcaagat	cctaccgga	aaggctcagt	3000
ggtcaatgtg	aatcctacca	acactaggcc	acagagtgac	accccgga	ttcgtaaata	3060
caagaagagg	tttaactctg	agattctgtg	tgctgcctta	tggggagtga	atttgctagt	3120
gggtacagag	agtggcctga	tgctgctgga	cagaagtggc	caaggggaagg	tctatcctct	3180
tatcaaccga	agacgatttc	aacaaatgga	cgtacttgag	ggcttgaatg	tcttggtgac	3240
aatatctggc	aaaaaggata	agttacgtgt	ctactatttg	tcctgggtta	gaaataaaat	3300
acttcacaat	gatccagaag	ttgagaagaa	gcagggatgg	acaaccgtag	gggatttgga	3360
aggatgtgta	cattataaag	ttgtaaaata	tgaaagaatc	aaatttctgg	tgattgcttt	3420
gaagagttct	gtggaagtct	atgcgtgggc	accaaagcca	tatcaciaat	ttatggcctt	3480
taagtcatth	ggagaattgg	tacataagcc	attactgggtg	gatctcactg	ttgaggaagg	3540
ccagagggtg	aaagtgatct	atggatcctg	tgctggattc	catgctgttg	atgtggattc	3600
aggatcagtc	tatgacattt	atctaccaac	acatatccag	tgtagcatca	aaccccatgc	3660
aatcatcatc	ctccccaata	cagatggaat	ggagcttctg	gtgtgctatg	aagatgaggg	3720
ggtttatgta	aacacatatg	gaaggatcac	caaggatgta	gttctacagt	ggggagagat	3780
gcctacatca	gtagcatata	ttcgatccaa	tcagacaatg	ggctggggag	agaaggccat	3840
agagatccga	tctgtggaaa	ctggtcactt	ggatgggtgtg	ttcatgcaca	aaagggctca	3900
aagactaaaa	ttcttgtgtg	aacgcaatga	caagggtgtc	tttgctctg	ttcgggtctgg	3960
tggcagcagt	caggtttatt	tcatgacctt	aggcaggact	tctcttctga	gctggtagaa	4020
gcagtgtgat	ccagggatta	ctggcctcca	gagtcttcaa	gatcctgaga	acttgggaatt	4080
ccttgtaact	ggagctcgga	gctgcaccga	gggcaaccag	gacagctgtg	tgtgcagacc	4140
tcatgtgttg	ggttctctcc	cctccttcc	gttctcttta	tataccagtt	tatccccatt	4200
cttttttttt	ttcttactcc	aaaataaatc	aaggctgcaa	tgacagctgg	gctgttcaga	4260

ttctaccatc aggtgctata agtgtttggg attgagcatc atactggaaa gcaaacacct	4320
ttcctccagc tccagaattc cttgtctctg aatgactctg tcttgtgggt gtctgacagt	4380
ggcgacgatg aacatgccgt tggttttatt ggcagtgggc acaaggaggt gagaagtgg	4440
ggtaaaagga gcggagtgtc gaagcagaga gcgatttaa tataagtaaca ttaacagtgt	4500
atttaattga ctttctttt ttgtaatgtg acgatatgtg gacaaagaag aagatgcagg	4560
tttaagaagt taatatttat aaaatgtgaa agacacagtt actaggataa cttttttgtg	4620
ggtggggcctt gggagatggg gtgggggtggg ttaaggggtc ccattttgtt tctttggatt	4680
tgggggtggg gtcttgcca agaactcagt ctttttctg tgtaccaggt tgcctaaatc	4740
atgtgcagat ggttctaaaa aaaaaaaaaa aaaaaaaaaa aaaaggaaaa aaaaaagaa	4800
aaagaaaacg tgtgcatttt gtataatggc cagaactttg tctgtgaca gtattagcac	4860
tgcctcagtt aaaggtttaa tttttgttta aacctagacg tgcaacaaaa gttttaccac	4920
agtctgcact tgcagaagaa agaaaaaaat tcaaaccaca tgtttatttt tttttgcct	4980
acctcattgt tcttaatgca ttgagaggtg atttagttta tatgtttttg gaagaaacca	5040
ttaatgttta atttaatctt aatacaaaaa cgaccagatt gaagtttgac ttttattgtc	5100
acaaatcagc aggcacaaga actgtccatg aagatgggaa atagccttaa ggctgatgca	5160
gtttacttac aagtttagaa accagaatgc tttgttttta ccagattcac cattagaggt	5220
tgatggggca actgcagccc atgacacaag atctcattgt tctcgatgta gaggggttg	5280
tagcagacag gtggttacat tagaatagtc acacaaactg ttcagtgttg caggaacctt	5340
ttcttggggg tgggggagtt tcccttttct aaaaatgcaa tgcactaaaa ctattttaag	5400
aatgtagtta attctgctta ttcataaagt gggcatcttc tgtgttttag gtgtaatatc	5460
gaagtcttg cttttctcgt tttctcactt gctctcttgt tctctgtttt tttaaaccaa	5520
ttttacttta tgaatatatt catgacattt gtaataaatg tcttgagaaa gaatttgttt	5580
catggcttca tggatcacac tcaagctccc gtaaggatat taccgtctca ggaaaggatc	5640
aggactccat gtcacagtcc tgccatctta ctttctctt gtcgagttct gagtggaaat	5700
aactgcatta tggctgcttt aacctcagtc atcaaaagaa acttgctgtt ttttaggctt	5760
gatctttttc ctttgtgggt aattttctctg tatattgtga aaatggggga ttttccctct	5820
gtccccccc acctaaacac agcagccatt tgtacctgtt tgcttcccat cccacttggc	5880
accactctg acctcttgtc agtttctgt tcttgggtcc atctttttga aaaaggccct	5940
cctttgagct acaaacatct ggtaagacaa gtacatccac tcatgaatgc agacacagca	6000
gctgggtggtt ttgtgtatac ctgtaaagac aagctgagaa gcttactttt tggggaagta	6060
aaagaagatg gaaatggatg tttcatttgt atgagtttg agcagtgtg aaggccaaag	6120

ccgcctactg	gtttgtagtt	aacctagaga	aggttgaaaa	attaatccta	ccttttaaagg	6180
gatttgaggt	aggctggatt	ccatcgccac	aggactttag	ttagaattaa	attcctgctt	6240
gtaatttata	tccatgttta	ggcttttcat	aagatgaaac	atgccacagt	gaacacactc	6300
gtgtacatat	caagagaaga	aggaaaggca	caggtggaga	acagtaaaag	gtgggcagat	6360
gtctttgaag	aaatgctcaa	tgtctgatgc	taagtgggag	aaggcagaga	acaaaggatg	6420
tggcataatg	gtcttaacat	tatccaaaga	cttgaagctc	catgtctgta	agtcaaagt	6480
tacacaaaaa	aaaatgcaaa	tgggtgttca	ttggaattac	caagtgttta	gaacttgctg	6540
gctttcccat	agggtgtaaa	ggggtctgag	ctcacaccga	gttgtgcttg	gcttgcttgt	6600
gcagctccag	gcacccggtg	ggcactctgg	tgggtgttgt	ggtgaactga	attgaatcca	6660
ttgttgggct	taagttactg	aaattggaac	accctttgtc	cttctcggcg	ggggcttcct	6720
ggctctgtgct	ttacttggct	tttttccttc	ccgtcttagc	ctcacccctt	tgtcaaccag	6780
attgagttgc	tatagcttga	tgcagggacc	cagtgaagtt	tctccgttaa	agattgggag	6840
tcgtcgaaat	gtttagattc	ttttaggaaa	ggaattat	ttcccccttt	tacagggtag	6900
taacttctcc	acagaagtgc	caatatggca	aaattacaca	agaaaacagt	attgcaatga	6960
caccattaca	taaggaacat	tgaactgtta	gaggagtgtc	cttccaaaca	aaacaaaaat	7020
gtctctaggt	ttagtcagag	ctttcacaa	taataacctt	tctgtattaa	aatcagagta	7080
accctttctg	tattgagtgc	agtgtttttt	actcttttct	catgcacatg	ttacgttgga	7140
gaaaatgttt	acaaaaatgg	ttttgttaca	ctaattgcgc	ccacatattt	atggtttatt	7200
ttaagtgact	ttttatgggt	tatttaggtt	ttcgtcttag	ttgtagcaca	cttaccctaa	7260
ttttgccaat	tattaatttg	ctaaatagta	atacaaatga	caaactgcat	taaatttact	7320
aattataaaa	gctgcaaagc	agactgggtg	caagtacaca	gccctttttt	ttgcagtgtc	7380
aacttgtcta	ctgtgtatta	tgaaaattac	tgttgtcccc	ccaccctttt	ttccttaa	7440
aaagtaaaaa	tgacacctaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaa	7495

<210> 17  
 <211> 7033  
 <212> DNA  
 <213> HUMAN

<400> 17						
cacagagcga	cagagacatt	tattgttatt	tgttttttgg	tggcaaaaag	ggaaaatggc	60
gaacgactcc	cctgcaaaaa	gtctgggtgga	catcgacctc	tcctccctgc	gggatcctgc	120
tgggattttt	gagctgggtg	aagtgggttg	aaatggcacc	tatggacaag	tctataaggg	180
tcgacatgtt	aaaacgggtc	agttggcagc	catcaaagtt	atggatgtca	ctgaggatga	240



agaggaagaa atcaaactgg agataaatat gctaaagaaa tactctcatc acagaaacat	300
tgcaacatat tatggtgctt tcatcaaaaa gagccctcca ggacatgatg accaactctg	360
gcttgttatg gagttctgtg gggctgggtc cattacagac cttgtgaaga acaccaaagg	420
gaacacactc aaagaagact ggatcgctta catctccaga gaaatcctga ggggactggc	480
acatcttcac attcatcatg tgattcacccg ggatatcaag ggccagaatg tgttgctgac	540
tgagaatgca gaggtgaaac ttgttgactt tgggtgtgagt gctcagctgg acaggactgt	600
ggggcggaga aatacgttca taggcactcc ctactggatg gtcctgagg tcatcgccctg	660
tgatgagaac ccagatgcc aatatgatta cagaagtgat ctttggtctt gtggcattac	720
agccattgag atggcagaag gtgctcccc tctctgtgac atgcatccaa tgagagcact	780
gtttctcatt cccagaaacc ctctccccg gctgaagtca aaaaaatggc cgaagaagtt	840
ttttagtttt atagaagggg gcctggtgaa gaattacatg cagcggccct ctacagagca	900
gcttttgaaa catcctttta taagggatca gccaaatgaa aggcaagtta gaatccagct	960
taaggatcat atagatcgta ccaggaagaa gagaggcgag aaagatgaaa ctgagtatga	1020
gtacagtggg agtgaggaag aagaggagga agtgcctgaa caggaaggag agccaagttc	1080
cattgtgaac gtgcctggtg agtctactct tcgccgagat ttcttgagac tgcagcagga	1140
gaacaaggaa cgttccgagg ctcttcggag acaacagtta ctacaggagc aacagctccg	1200
ggagcaggaa gaatataaaa ggcaactgct ggcagagaga cagaagcgga ttgagcagca	1260
gaaagaacag aggcgacggc tagaagagca acaaaggaga gagcgggaag ctagaaggca	1320
gcaggaacgt gaacagcgaa ggagagaaca agaagaaaag aggcgtctag aggagttgga	1380
gagaaggcgc aaagaagaag aggagaggag acgggcagaa gaagaaaaga ggagagttga	1440
aagagaacag gagtatatca ggcgacagct agaagaggag cagcggcact tggaagtcct	1500
tcagcagcag ctgctccagg agcaggccat gttactgcat gaccatagga ggccgcaccc	1560
gcagcactcg cagcagccgc caccaccgca gcaggaaagg agcaagccaa gcttccatgc	1620
tcccagagccc aaagcccact acgagcctgc tgaccgagcg cgagaggttc ctgtgagaac	1680
aacatctcgc tcccctgttc tgtcccgtcg agattcccca ctgcagggca gtgggcagca	1740
gaatagccag gcaggacaga gaaactccac cagcagtatt gagcccaggc ttctgtggga	1800
gagagtggag aagctggtgc ccagacctgg cagtggcagc tcctcagggt ccagcaactc	1860
aggatcccag cccgggtctc accctgggtc tcagagtggc tccggggaac gcttcagagt	1920
gagatcatca tccaagtctg aaggctctcc atctcagcgc ctggaaaatg cagtaaaaa	1980
acctgaagat aaaaagggaag ttttcagacc cctcaagcct gctggcgaag tggatctgac	2040

cgcaactggcc	aaagagcttc	gagcagtgga	agatgtacgg	ccacctcaca	aagtaacgga	2100
ctactcctca	tccagtgagg	agtcggggac	gacggatgag	gaggacgacg	atgtggagca	2160
ggaaggggct	gacgagtcca	cctcaggacc	agaggacacc	agagcagcgt	catctctgaa	2220
tttgagcaat	ggtgaaacgg	aatctgtgaa	aaccatgatt	gtccatgatg	atgtagaaag	2280
tgagccggcc	atgaccccat	ccaaggaggg	cactctaata	gtccgccaga	ctcagtcgcg	2340
tagtagcaca	ctccagaaac	acaaatcttc	ctcctccttt	acacctttta	tagaccccag	2400
attactacag	atttctccat	ctagcggaac	aacagtgaca	tctgtggtgg	gattttcctg	2460
tgatgggatg	agaccagaag	ccataaggca	agatcctacc	cggaaaggct	cagtgggtcaa	2520
tgtgaatcct	accaacacta	ggccacagag	tgacaccccg	gagattcgta	aatacaagaa	2580
gaggtttaac	tctgagattc	tgtgtgctgc	cttatgggga	gtgaatttgc	tagtgggtac	2640
agagagtggc	ctgatgctgc	tggacagaag	tggccaaggg	aaggtctatc	ctcttatcaa	2700
ccgaagacga	tttcaacaaa	tggacgtact	tgagggcttg	aatgtcttgg	tgacaatatc	2760
tggcaaaaag	gataagttac	gtgtctacta	tttgtcctgg	ttaagaaata	aaataacttca	2820
caatgatcca	gaagttgaga	agaagcaggg	atggacaacc	gtaggggatt	tggaaggatg	2880
tgtacattat	aaagttgtaa	aatatgaaag	aatcaaattt	ctggtgattg	ctttgaagag	2940
ttctgtggaa	gtctatgcgt	gggcaccaa	gccatatcac	aaatttatgg	cctttaagtc	3000
at ttggagaa	ttggtacata	agccattact	ggtggatctc	actgttgagg	aaggccagag	3060
gttgaaagtg	atctatggat	cctgtgctgg	attccatgct	gttgatgtgg	attcaggatc	3120
agtctatgac	atttatctac	caacacatgt	aagaaagaac	ccacactcta	tgatccagtg	3180
tagcatcaaa	ccccatgcaa	tcatcatcct	ccccaataca	gatggaatgg	agcttctggt	3240
gtgctatgaa	gatgaggggg	tttatgtaaa	cacatatgga	aggatcacca	aggatgtagt	3300
tctacagtgg	ggagagatgc	ctacatcagt	agcatatatt	cgatccaatc	agacaatggg	3360
ctggggagag	aaggccatag	agatccgatc	tgtggaaact	ggtcacttgg	atggtgtgtt	3420
catgcacaaa	agggctcaaa	gactaaaatt	cttgtgtgaa	cgcaatgaca	aggtgttctt	3480
tgccctctgtt	cgggtctggtg	gcagcagtca	ggtttatctt	atgaccttag	gcaggacttc	3540
tcttctgagc	tggtagaagc	agtgtgatcc	agggattact	ggcctccaga	gtcttcaaga	3600
tcctgagaac	ttggaattcc	ttgtaactgg	agctcggagc	tgacccgagg	gcaaccagga	3660
cagctgtgtg	tgcagacctc	atgtgttggg	ttctctcccc	tccttctgtg	tcctcttata	3720
taccagttta	tccccattct	tttttttttt	cttactccaa	aataaatcaa	ggctgcaatg	3780
cagctggtgc	tgttcagatt	ctaccatcag	gtgctataag	tgtttgggat	tgagcatcat	3840
actggaaagc	aaacaccttt	cctccagctc	cagaattcct	tgtctctgaa	tgactctgtc	3900

ttgtgggtgt	ctgacagtgg	cgacgatgaa	catgccgttg	gttttattgg	cagtgggcac	3960
aaggaggtga	gaagtgggtg	taaaaggagc	ggagtgctga	agcagagagc	agatttaata	4020
tagtaacatt	aacagtgtat	ttaattgaca	tttctttttt	gtaatgtgac	gatatgtgga	4080
caaagaagaa	gatgcaggtt	taagaagtta	atatttataa	aatgtgaaag	acacagttac	4140
taggataact	tttttgtggg	tggggcttgg	gagatggggg	gggggtgggtt	aaggggtccc	4200
attttgtttc	tttggatttg	gggtgggggt	cctggccaag	aactcagtca	tttttctgtg	4260
taccaggttg	cctaaatcat	gtgcagatgg	ttctaaaaaa	aaaaaaaaaa	aaaaaaaaaa	4320
aaggaaaaaa	aaaaagaaaa	agaaaacgtg	tgcattttgt	ataatggcca	gaactttgtc	4380
gtgtgacagt	attagcactg	cctcagttaa	aggtttaatt	tttgtttaaa	cctagacgtg	4440
caacaaaagt	tttaccacag	tctgcacttg	cagaagaaag	aaaaaaattc	aaaccacatg	4500
tttatttttt	ttttgcctac	ctcattgttc	ttaatgcatt	gagaggtgat	ttagtttata	4560
tgtttttgga	agaaaccatt	aatgtttaat	ttaatcttaa	taccaaacg	accagattga	4620
agtttgactt	ttattgtcac	aaatcagcag	gcacaagaac	tgtccatgaa	gatgggaaat	4680
agccttaagg	ctgatgcagt	ttacttacia	gtttagaaac	cagaatgctt	tgtttttacc	4740
agattcacca	ttagaggttg	atggggcaac	tgcagcccat	gacacaagat	ctcattgttc	4800
tcgatgtaga	ggggttggtg	gcagacaggt	ggttacatta	gaatagtcac	acaaactggt	4860
cagtgttgca	ggaacctttt	cttgggggtg	ggggagtttc	cctttttctaa	aaatgcaatg	4920
cactaaaact	attttaagaa	tgtagttaat	tctgcttatt	cataaagtgg	gcatcttctg	4980
tgtttttaggt	gtaatatcga	agtcctggct	tttctcgttt	tctcacttgc	tctcttggtc	5040
tctgtttttt	taaaccaatt	ttactttatg	aatatattca	tgacatttgt	aataaatgtc	5100
ttgagaaaga	atttgtttca	tggcttcatg	gtcatcactc	aagctcccgt	aaggatatta	5160
ccgtctcagg	aaaggatcag	gactccatgt	cacagtctctg	ccatcttact	ttcctcttgt	5220
cgagttctga	gtggaaataa	ctgcattatg	gctgctttta	cctcagtcac	caaaagaaac	5280
ttgctgtttt	ttaggcttga	tctttttcct	ttgtgggtta	ttttcctgta	tattgtgaaa	5340
atgggggatt	ttccctctgc	tcccaccac	ctaaacacag	cagccatttg	tacctgtttg	5400
cttcccatcc	cacttggcac	ccactctgac	ctcttgctag	tttcctgttc	ctgggtccat	5460
ctttttgaaa	aaggccctcc	tttgagctac	aaacatctgg	taagacaagt	acatccactc	5520
atgaatgcag	acacagcagc	tgggtggttt	gtgtatacct	gtaaagacaa	gctgagaagc	5580
ttactttttg	gggaagtaaa	agaagatgga	aatggatggt	tcatttgtat	gagtttggag	5640
cagtgttgaa	ggccaaagcc	gcctactggg	ttgtagttaa	cctagagaag	gttgaaaaat	5700

taatcctacc	tttaaagga	tttgaggtag	gctggattcc	atcgccacag	gacttttagtt	5760
agaattaaat	tcttgcttgt	aatttatatc	catgtttagg	cttttcataa	gatgaaacat	5820
gccacagtga	acacactcgt	gtacatatca	agagaagaag	gaaaggcaca	ggtggagAAC	5880
agtaaaaggt	gggcagatgt	ctttgaagaa	atgctcaatg	tctgatgcta	agtgggagaa	5940
ggcagagAAC	aaaggatgtg	gcataatggt	cttaacatta	tccaaagact	tgaagctcca	6000
tgtctgtaag	tcaaatgtta	cacaaaaaaaa	aatgcaaatg	gtgtttcatt	ggaattacca	6060
agtgccttaga	acttgctggc	tttcccatag	gtggtaaagg	ggtctgagct	cacaccgagt	6120
tgtgcttggc	ttgcttgctg	agctccaggc	acccggtggg	cactctggtg	gtgtttgtgg	6180
tgaactgaat	tgaatccatt	gttgggctta	agttactgaa	attggaacac	cctttgtcct	6240
tctcggcggg	ggcttctctg	tctgtgcttt	acttggcttt	tttcttccc	gtcttagcct	6300
caccccttg	tcaaccagat	tgagttgcta	tagcttgatg	cagggacca	gtgaagtttc	6360
tccgttaaag	attgggagtc	gtcgaaatgt	ttagattctt	ttaggaaagg	aattattttc	6420
cccccttta	cagggtagta	acttctccac	agaagtgccA	atatggcaaa	attacacaag	6480
aaaacagtat	tgcaatgaca	ccattacata	aggaacattg	aactgttaga	ggagtgtctc	6540
tccaaacaaa	acaaaaatgt	ctctagggtt	agtcagagct	ttcacaagta	ataacctttc	6600
tgtattaaaa	tcagagtaac	cctttctgta	ttgagtgcag	tgttttttac	tcttttctca	6660
tgcacatgtt	acgttggaga	aaatgtttac	aaaaatgggt	ttgttacact	aatgcgcacc	6720
acatatttat	ggtttatttt	aagtgacttt	ttatgggtta	tttaggtttt	cgtcttagtt	6780
gtagcacact	taccctaatt	ttgccaatA	ttaatttgct	aaatagtaat	acaaatgaca	6840
aactgcatta	aatttactaa	ttataaaagc	tgcaaagcag	actggtggca	agtacacagc	6900
cctttttttt	gcagtgttaa	cttgtctact	gtgtattatg	aaaattactg	ttgtcccccc	6960
accctttttt	ccttaaataa	agtaaaaatg	acacctaAAA	aaaaaaaaaa	aaaaaaaaaa	7020
aaaaaaaaaa	aaa					7033

<210> 18  
 <211> 3792  
 <212> DNA  
 <213> HUMAN

<400> 18	
atggcgAACg	actccctgc
aaaaagtctg	gtggacatcg
acctctcctc	cctgcgggat
60	
cctgctggga	tttttgagct
ggtggaagtg	gttggaaatg
gcacctatgg	acaagtctat
120	
aagggtcgac	atgttaaaac
gggtcagttg	gcagccatca
aagttagga	tgtcactgag
180	
gatgaagagg	aagaaatcaa
actggagata	aatatgctaa
agaaatactc	tcatcacaga
240	

aacattgcaa catattatgg tgctttcatc aaaaagagcc ctccaggaca tgatgaccaa	300
ctctggcttg ttatggagtt ctgtggggct ggggccatta cagaccttgt gaagaacacc	360
aaagggaaaca cactcaaaga agactggatc gcttacatct ccagagaaat cctgagggga	420
ctggcacatc ttcacattca tcatgtgatt caccgggata tcaagggcca gaatgtgttg	480
ctgactgaga atgcagaggt gaaacttggt gactttggtg tgagtgtca gctggacagg	540
actgtggggc ggagaaatac gttcataggc actccctact ggatggctcc tgaggctatc	600
gcctgtgatg agaaccaga tgccacctat gattacagaa gtgatctttg gtcttggtgc	660
attacagcca ttgagatggc agaaggtgct cccctctct gtgacatgca tccaatgaga	720
gcactgtttc tcattcccag aaacctcct ccccggtga agtcaaaaa atggtcgaag	780
aagtttttta gttttataga agggtgctg gtgaagaatt acatgcagcg gccctctaca	840
gagcagcttt tgaacatcc ttttataagg gatcagccaa atgaaaggca agttagaatc	900
cagcttaagg atcatataga tcgtaccagg aagaagagag gcgagaaaga tgaaactgag	960
tatgagtaca gtgggagtga ggaagaagag gaggaagtgc ctgaacagga aggagagcca	1020
agttccattg tgaacgtgcc tgggtgagtct actcttcgcc gagatttcct gagactgcag	1080
caggagaaca aggaacgttc cgaggctctt cggagacaac agttactaca ggagcaacag	1140
ctccgggagc aggaagaata taaaaggcaa ctgctggcag agagacagaa gcggattgag	1200
cagcagaaag aacagaggcg acggctagaa gagcaacaaa ggagagagcg ggaagctaga	1260
aggcagcagg aacgtgaaca gcgaaggaga gaacaagaag aaaagaggcg tctagaggag	1320
ttggagagaa ggcgcaaaga agaagaggag aggagacggg cagaagaaga aaagaggaga	1380
gttgaaagag aacaggagta tatcaggcga cagctagaag aggagcagcg gcacttgga	1440
gtccttcagc agcagctgct ccaggagcag gccatgttac tggagtgccg atggcgggag	1500
atggaggagc accggcaggc agagaggctc cagaggcagt tgcaacaaga acaagcatat	1560
ctcctgtctc tacagcatga ccataggagg ccgcacccgc agcactcgca gcagccgcca	1620
ccaccgcagc aggaaggag caagccaagc ttccatgctc ccgagcccaa agcccactac	1680
gagcctgctg accgagcgcg agagggtgaa gatagattta ggaaaactaa ccacagctcc	1740
cctgaagccc agtctaagca gacaggcaga gtattggagc caccagtgc ttcccgatca	1800
gagtcttttt ccaatggcaa ctccgagtct gtgcatcccg ccctgcagag accagcggag	1860
ccacaggttc ctgtgagaac aacatctcgc tcccctgttc tgtcccgctc agattcccca	1920
ctgcagggca gtgggcagca gaatagccag gcaggacaga gaaactccac cagtattgag	1980
cccaggcttc tgtgggagag agtgagaaag ctgggtgcca gacctggcag tggcagctcc	2040
tcagggtcca gcaactcagg atcccagccc gggctctacc ctgggtctca gagtggctcc	2100

ggggaacgct tcagagtgag atcatcatcc aagtctgaag gctctccatc tcagcgctg	2160
gaaaatgcag tgaaaaaacc tgaagataaa aaggaagttt tcagaccct caagcctgct	2220
gatctgaccg cactggccaa agagcttcga gcagtgggaag atgtacggcc acctcacaaa	2280
gtaacggact actcctcatc cagtgaggag tcggggacga cggatgagga ggacgacgat	2340
gtggagcagg aaggggctga cgagtccacc tcaggaccag aggacaccag agcagcgtca	2400
tctctgaatt tgagcaatgg tgaaacggaa tctgtgaaaa ccatgattgt ccatgatgat	2460
gtagaaagtg agccggccat gaccccatcc aaggagggca ctctaatacgt ccgccggact	2520
cagtccgcta gtagcacact ccagaaacac aaatcttcct cctcctttac accttttata	2580
gacccagat tactacagat ttctccatct agcggaacaa cagtgcacatc tgtggtggga	2640
ttttcctgtg atgggatgag accagaagcc ataaggcaag atcctaccg gaaaggctca	2700
gtggtcaatg tgaatcctac caacactagg ccacagagtg acaccccga gattcgtaaa	2760
tacaagaaga ggtttaactc tgagattctg tgtgctgcct tatggggagt gaatttgcta	2820
gtgggtacag agagtggcct gatgctgctg gacagaagtg gccaaaggaa ggtctatcct	2880
cttatcaacc gaagacgatt tcaacaaatg gacgtacttg agggcttgaa tgtcttggtg	2940
acaatatctg gcaaaaagga taagttacgt gtctactatt tgtcctggtt aagaaataaa	3000
atacttcaca atgatccaga agttgagaag aagcagggat ggacaaccgt aggggatttg	3060
gaaggatgtg tacattataa agttgtaaaa tatgaaagaa tcaaatttct ggtgattgct	3120
ttgaagagtt ctgtggaagt ctatgcgtgg gcaccaaagc catatcacia atttatggcc	3180
tttaagtcat ttggagaatt ggtacataag ccattactgg tggatctcac tgttgaggaa	3240
ggccagaggt tgaaagtgat ctatggatcc tgtgctggat tccatgctgt tgatgtggat	3300
tcaggatcag tctatgacat ttatctacca acacatatcc agtgtagcat caaaccccat	3360
gcaatcatca tcctcccaa tacagatgga atggagcttc tgggtgtgcta tgaagatgag	3420
ggggtttatg taaacacata tggaaggatc accaaggatg tagttctaca gtggggagag	3480
atgcctacat cagtagcata tattcgatcc aatcagacaa tgggctgggg agagaaggcc	3540
atagagatcc gatctgtgga aactggtcac ttggatgggtg tgttcatgca caaaagggct	3600
caaagactaa aattcttggtg tgaacgcaat gacaagggtg tctttgcctc tgttcggctc	3660
gggtggcagca gtcaggttta ttcatgacc ttaggcagga cttctcttct gagctggtag	3720
aagcagtgtg atccagggat tactggcctc cagagtcttc aagatcctga gaacttgga	3780
ttccttgtaa ct	3792

<210> 19

<211> 3095  
 <212> DNA  
 <213> HUMAN

<400> 19

```

gcccgcaggg ttcttccaag atggcggcgc agaggaggag cttgctgcag agtgagcagc      60
agccaagctg gacagatgac ctgcctctct gccacctctc tgggggtggc tcagcctcca      120
accgcagcta ctctgctgat ggcaagggca ctgagagcca cccgccagag gacagctggc      180
tcaagttcag gagtgagaac aactgcttcc tgtatggggc cttcaacggc tatgatggca      240
accgagtgac caacttcgtg gcccagcggc tgtccgcaga gctcctgctg ggccagctga      300
atgccgagca cgccgaggcc gatgtgcggc gtgtgctgct gcaggccttc gatgtggtgg      360
agaggagctt cctggagtcc attgacgacg ccttggctga gaaggcaagc ctccagtcgc      420
aattgccaga gggagtccct cagcaccagc tgcctcctca gtatcagaag atccttgaga      480
gactcaagac gttagagagg gaaatttcgg gaggggcat ggccgttgtg gcggtccttc      540
tcaacaacaa gctctacgtc gccaatgtcg gtacaaaccg tgcactttta tgcaaatcga      600
cagtggatgg gttgcaggtg acacagctga acgtggacca caccacagag aacgaggatg      660
agctcttccg tctttcgcag ctgggcttgg atgctggaaa gatcaagcag gtggggatca      720
tctgtgggca ggagagcacc cggcggatcg gggattacaa ggttaaatat ggctacacgg      780
acattgacct tctcagcgtc gccaaagtcca aaccaatcat cgcagagcca gaaatccatg      840
gggcacagcc gctggatggg gtgacgggct tcttgggtgct gatgtcggag gggttgtaca      900
aggccctaga ggcagcccat gggcctgggc aggccaacca ggagattgct gcgatgattg      960
aactgagtt tgccaagcag acctccctgg acgcagtggc ccaggccgtc gtggaccggg     1020
tgaagcgcac ccacagcgac accttcgcca gtgggtgggga gcgtgccagg ttctgcccc     1080
ggcacgagga catgaccctg ctagtgagga actttggcta cccgctgggc gaaatgagcc     1140
agcccacacc gagcccagcc ccagctgcag gaggacgagt gtaccctgtg tctgtgccat     1200
actccagcgc ccagagcacc agcaagacca gcgtgaccct ctcccttgct atgccctccc     1260
agggccagat ggtcaacggg gctcacagtg cttccaccct ggacgaagcc acccccaccc     1320
tcaccaacca aagcccgacc ttaaccctgc agtccaccaa cacgcacacg cagagcagca     1380
gctccagctc tgacggaggc ctcttcctgt cccggcccgcc cactcgtct cgcctggcg     1440
aggacggtcg tgttgagccc tatgtggact ttgctgagtt ttaccgcctc tggagcgtgg     1500
accatggcga gcagagcgtg gtgacagcac cgtagggcag ccggaggaat gcagcccaag     1560
cagggcctgg catggggcag gacagggctc agccttttcc taacatctgc ctgtgccaca     1620
acggccagca ggtgccccat cctctgccca cagcagactc tgtcccatgg ctctccgggc     1680

```

agtagagtgt	gtgagtgcag	actggacctg	tggttcatat	cttgtcacca	cccggaagc	1740
tgaaggccac	ttcctcccag	atggcctcag	ccaggaccat	cgccctttct	cagagcagag	1800
ggccaggtag	ggaaaccgca	gtgggcctgc	aagccgccc	agcctcccca	gcagcctcct	1860
acagagcagg	aagaggcgcc	ctgtgaaccc	tgtagtgttg	caggcccagc	agaccctgct	1920
gtcccaagcc	cacccctcct	cccaccatca	cctccctcac	ctcgggacag	tagccctcca	1980
cttctccagc	ctctcagccc	tgtgctcctg	tatccagagt	ggaaccagg	ctggtgtccg	2040
tatctgtccc	tgggccccac	ccctggacct	gccttggttg	tgtcatctgt	tgtaaacatt	2100
ccaggaggac	caggggagca	tctggggcct	gggatggcca	cagaaggggc	aggccagggtg	2160
gaaaggagcc	agggggaagt	ggtctaagag	acctggaact	gccagaggat	ggcggcctgg	2220
gcttccccag	agccaggcgt	gcgggagagg	tgaggactgg	ccccggtggg	ctgaggcagg	2280
ggccgctgtc	gtcaggcctg	agccagggtg	agctgggtgc	tgccttgctt	cttccttctg	2340
gtgctgtgaa	gaccataggc	tggcaggcag	ctgagatgaa	ctgtctttac	cactgatgag	2400
gggcctctgc	cggctgaggg	tagcaagcag	gggttggtgag	tcaggctggg	ggacttgttt	2460
gaaagaaaga	ggagtggaa	tgtggttccc	aggagggaag	aggttccttt	gagacacagt	2520
aaccctggga	ggcataggag	aagggtcggg	ccagcccagc	ccagggcctg	agttagacta	2580
tttcccacat	gttctctgcc	ttcagtgggg	agggggtgcc	accagggtg	tcggccagga	2640
ttgccactcc	tgtttcagag	gaagcaggcc	gagagacttg	caccttggac	aagccacaca	2700
atcagtgggg	cagccagagc	tcagacctga	gccattgtgt	cagtatccag	gacccccgg	2760
attctccacg	ccctccccat	ctcccagtct	ccctgcccc	catgccccag	accggcccac	2820
cagggactag	ccgctgtcgc	acagcctctg	gggtgcttg	tctctgcaaa	gtcaaaggcc	2880
tgacagctct	gtggcctggg	aatccatttt	cctgcgggag	agcagggcct	ggtgtggaac	2940
cagggagctg	tgggaagcca	cagcagaaat	ggaagaaaaa	caggtctcag	cccagggtcc	3000
tcgctcactc	cctcactccc	cactttgaag	ccatctctgt	tctgcagggtg	agaggattta	3060
aagtcagtca	caaaggcttg	ggaacaaaag	gaatt			3095

<210> 20  
 <211> 1412  
 <212> DNA  
 <213> HUMAN

<400> 20	
attaattgct	tgccatcatg agcagaagca agcgtgacaa caatttttat agtgtagaga 60
ttggagattc	tacattcaca gtcctgaaac gatatcagaa tttaaaacct ataggctcag 120
gagctcaagg	aatagtatgc gcagcttatg atgccattct tgaaagaaat gttgcaatca 180



agaagctaag ccgaccattt cagaatcaga ctcatgccaa gcgggcctac agagagctag	240
ttcttatgaa atgtgttaat cacaaaaata taattggcct tttgaatgtt ttcacaccac	300
agaaatccct agaagaattt caagatgttt acatagtcac ggagctcatg gatgcaaadc	360
tttgccaagt gattcagatg gagctagatc atgaaagaat gtcctacctt ctctatcaga	420
tgctgtgtgg aatcaagcac cttcattctg ctggaattat tcatcgggac ttaaagccca	480
gtaatatagt agtaaaatct gattgcactt tgaagattct tgacttcggg ctggccagga	540
ctgcaggaac gagttttatg atgacgcctt atgtagtgac tcgctactac agagcaccgc	600
aggctcatct tggcatgggc tacaaggaaa acgtggattt atgggtctgtg ggggtgcatta	660
tgggagaaat ggtttgccac aaaatcctct ttccaggaag ggactatatt gatcagtggg	720
ataaagttat tgaacagctt ggaacaccat gtcctgaatt catgaagaaa ctgcaaccaa	780
cagtaaggac ttacgttgaa aacagacctt aatatgctgg atatagcttt gagaaactct	840
tccctgatgt ccttttccca gctgactcag aacacaacaa acttaaagcc agtcaggcaa	900
gggatttggt atccaaaatg ctggtaatag atgcatctaa aaggatctct gtagatgaag	960
ctctccaaca cccgtacatc aatgtctggg atgacacctt tgaagcagaa gctccaccac	1020
caaagatccc tgacaagcag ttagatgaaa gggaacacac aatagaagag tggaaagaat	1080
tgatatataa ggaagttatg gacttggagg agagaaccaa gaatggagtt atacgggggc	1140
agccctctcc tttaggtgca gcagtgatca atggctctca gcatccatca tcatcgtcgt	1200
ctgtcaatga tgtgtcttca atgtcaacag atccgacttt ggcctctgat acagacagca	1260
gtctagaagc agcagctggg cctctgggct gctgtagatg actacttggg ccatcggggg	1320
gtgggagggg tggggagtcg gttagtcatt gatagaacta ctttgaaaac aattcagtgg	1380
tcttatTTTT ggggtgatttt tcaaaaaatg ta	1412

<210> 21  
 <211> 20  
 <212> DNA  
 <213> HUMAN

<400> 21	
cctgggctgc cggctcgagc	20

<210> 22  
 <211> 20  
 <212> DNA  
 <213> HUMAN

<400> 22	
cgagctcggc cgtcgggtcc	20

<210> 23  
<211> 20  
<212> DNA  
<213> HUMAN

<400> 23  
cgtttacgtc gccgtccagc

20

<210> 24  
<211> 23  
<212> PRT  
<213> ARTIFICIAL SEQUENCE

<400> 24

Lys Lys Lys Val Ser Arg Ser Gly Leu Tyr Arg Ser Pro Ser Met Pro  
1 5 10 15

Glu Asn Leu Asn Arg Pro Arg  
20